

## FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC  
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCAACCCGAGG  
AGCAGCTCCTGCCCTGTCCGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGTTGTTGGCAGTGGGCGGCACAGAGCAGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC  
CGCCGAGCCCTGGGCTGGCCCTGCCAGGCCCTCGCTACGCGTGTGCCCCGGCTGGAAGAG  
GACCAGCGGCTTCTTGGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGACAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC  
CGGCAGTTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTC  
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG  
CTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTGC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTTTTCTCCTC  
CCCTTCCCTCGGGAGGGTCCCAGACCTTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCTTGGTTACCCCAACGGCATCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGCCTCAGTGGGGGCTGTGCTGACCCCCAGCACATAAAATGAAA  
CGTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTTATTGACGCTTATAATGTT  
TACAAAT

## **FIGURE 2**

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLLTTCDGHACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

## FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCTCCCCGCAGAGTCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCACGGCGGGGACTATGGTGAAATTCGCGCGCTCACGCCTACTGGCCCTGATC  
CGGTTCTTGTGTCCTCGGCGATCACCAACATAGCCATCGACTTCGGGGAGCAGGCGCTTGAA  
CGGGGGCATGTCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGACTTCAAAATGTGGGCTGTGTGTTT  
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC  
TGCCGTCTTTTACACACTGATAGCTTATAGTGATTTAGGATACACTATTCAATAAACTGCG  
ACCATGTGGACGAGTCGTGGGGAGCAAGACGAGAAGGGCCTTCTGTACTCTCGCGCCCTTT  
CCTTTCATGGACGAATGGCATGGACCCATGCTGGCATTCTTTAAACACAAATACAGTTT  
CTGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCGGGAGCCCCGTGCTCATCCCGATCCTCTCCTGTGACATGGGC  
GCACCTGTGCGCTGCACCAACCTGTGCTGGGCTACTACAAGAACATTACGACATCATCCC  
TGACAGAAGTGGCCCCGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTGTGACAGCCACATA  
CCCTGTGGGTTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCTGCTTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCACGCCCATC  
AAGAAGTTCACCTTCTGCTGTCATGGCTCTGTCACTCAGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACTGCTGTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCCTTTGACAGAAC  
TCTGTTGTTGCTTGGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTGCG  
GATCATGCTCTCATGCCAGCCTCGTGGTCTACCCCTACCTGGGGGTGCACGGTGCAGCC  
TGGCGTGGGCTCCCTCTGGCGGGCTTTGTGGGAGAATCCACATGTCGCCATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCTGGGAAATGAGAGG  
AGAATGAATAAAGGCACGGGACGCCATGGGCCTGACGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTTCCCTCTCCCATCGTATTTGTTCCTTTTTTTGTTTTGTTTTGTTAAT  
GAAAGAGCCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATATGGGTATGCTCACACT  
GACGGGGGACCTAGTGAAATGGTCTTTACTGTTGCTATGTGTAACCAACGAAACAACTGAC  
TTCATACCCCTGCCTCACGAAACCCAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
TCTCCCTGGACAATCTCCTCTTGGAAACCAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
CACCTTGCACAGCGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAACCTCGGCTTCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGACG  
GAGGCGGGTGGCAGCTGCAGCCCGAGTCCCGTTCACACTGAGGAACGGAGACCTGTGAC  
CACAGAGGCTGACAGATGGAAGAATCTCCCGTAGAAGGTTTGGTTTTGAAATGCCCCGGG  
GGCAGCAAACTGACATGTTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
GCTGTGAGTTCTCACCCTCCCGTGTATATACATGAGCTAACTTTTTTAAATTTGACAAA  
GCGCATCTCAGATTCCAGACCTGCGCATGACTTTTCTGAAGGCTGTGCTTTTCCCTCGC  
CTTTCTGAAGGTGCGATTAGAGCGAGTCACATGGAGCATCTAACTTTGCATTTTAGTTTT  
TACAGATCTGAAGCTTTAAGTCTCATCGACATTCTAATGCCAGGTTGCTGTAGGTGAAC  
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAAGCAAGACATTTTATAACG  
ATGACAGAGTCACTATGTGGTCTCCTGAAATAACGCATTGAAATCCATGCAAGTCAGTA  
TATTTTTCTAAGTTTTTGAAAGCAGGTTTTTCTCTTTAAAAAAATATAGACACGGTTCACT  
AAATTTGATTTAGTCAGAATCTTAGCTGAAAGAACCTTAAACAAAAAATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAAATTTATTTTAGGCTATAATACATTTTCTATTTTCG  
ATTTTCAATAAAATGTCTCTAATACAAAAAA

## **FIGURE 4**

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSEDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIIINKLHHVDESV  
GSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFAILLHSHLEC  
REPLLIPILSLYMGALVRCCTTLC LGYYKNIHDII PDRSGPELGGDATIRKMLSFWWPLALIL  
ATQRI SRPIVNL FVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSENTVTAHHKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR  
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLl  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEEVTDIVEMREENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

## **FIGURE 5**

CCTGACAGAAGTGCCCCGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT  
CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGTC

## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTCGGATTTTCT  
CCTTTTCCAGTTCCAGTCACAGNGAGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATTGTCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCACCCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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## **FIGURE 7**

TATTCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGAACTGAAGAAA  
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCCTACCTGGGGGTGCACGGTGAGAC

09078191.101503

## FIGURE 8

GCCCCGCGCCCCGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCTGCTCTGCGGCTCTGCCCTGCATCCTGTGCA  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTCTTCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT  
TCTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCCTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTCTTCA  
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGG  
AAGGCCGAGGAGTGCATTCCTGCTGCTGACGAGGCCTTCTTCTTCTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCCGAGGGCT  
GCCACGAGGGCAAGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCTGCCCAAGGTCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTCAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCATTTTGCCAAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCGAGCATTGTGGGCCCTCATCATCTTCTCCTGTGCACCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAAGTGAACAGCCTGATGCAGACCAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCTGTGTGCT  
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCAGCTTCAGCTTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACT  
GCCCCCTCCCAACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG  
CCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTTCTCTTCCCTCTCCTCTGT  
TGCCCATCTCAGCATCTCGGATGAAAGGGCTCCCTTGCTCTCAGGCTCCACGGGAGCGGG  
CTGCTGGAGAGAGCGGGGAACCTCCACACAGTGGGGCATCCGGCACTGAAGCCTTGGTGT  
CCTGGTCACTGCTCCCCAGGGGACCCCTGCCCTTCTCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAAAAAAA

## **FIGURE 9**

MGACLGACSLSCASCSCGSA PCILCSCCPASRNSTVSR LI FTFFLFLGLVLSIIMLSPGVE  
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAA FFFFTLLMLCVSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIW FYFGVVG SFLFILIQLVLLIDFAHSW  
NQRWLGAEECD SRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNL TFC  
VCVSIAAVLPKVQDAQPN SGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQOQQQQQVA  
ACEGRAFDNEQDGV TYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS  
WAGLLLYLWTLVAPLLLLNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTG  
AAATGCAACGATTCTCACCTCGTACAGTTACGCTCTCCCGGGCACGTCCGCGAGGACTTGA  
AGTCTTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG  
TGACTGCCGATTCCGAAGTCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCTGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA  
GCTGTACGGGAAGTCTTTTATAGGATAAACGTAGGCCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTCAGGAAAGAAAAAGAAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA  
GAGTGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACCTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTTCTTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCACCTAGATTTTAA  
GCAGTAAATAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

## **FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPFPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLFPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETIYHNRFDVQSAH  
RAATRGFIRYGWRGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPNPSVIDKQDKD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 76-96 and 171-195

#### **N-glycosylation site:**

amino acids 153-156

090701-140000

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG  
GCTGGCGCCGAACC

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TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATTGGAGTGCCGCCACCGGCACC CGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTGTCTGCCAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTTCATGNTAAACAACATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TACC

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GAGCGCCGCGCGCGCGCGCGCGCGCACTGCAGCCCCAGGGCCCCGGCCCCCACCACGCTT  
GCGTTGCTGCCCCGCGCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAAGGAACCT  
CCGCCGAGTGCAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGCGTTTGC  
GCTTCGCGTGTCTTCAAGAACTGCCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGTCATTGCAGTGGGCATCTTCTGTTCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAACAAATCATCAGGTGTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTAT  
GTTTCAGTTTTCTGTATCTTGCCTTGTGTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTAAACCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCGCGCGCAATCTAGTGCAATTCCTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCGTATTATGATCTTGTCTACTTCTGTAATTTCTGTTAAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACATCATCTGGAAAGTACCTTATTGATAGTGGCAATTATATATTTTTACT  
CTATGTTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCAATTGTCGGGCACGTGCCACTGTGGCCTT  
TCTTAGCATTTTTTACCTGCAGAAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGGAAAAAGAGTGGAATTTATTAATAACAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCTCAATTTTTTTTGGTCTTTTATGAAAGATTGTTGTGGTAAAAAGTGTAGTA  
TAAAAATGATAATTACTGTAGTCTTTTATGATTACACCAATGTATCTAGAAATAGTTAT  
GTC'TTAGGAAATGTGTTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCCAGTGACAAAAAGATATTTG  
ATTATCTTAAAAAATGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACGCAACTT  
GCTCAAACTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATGGAATCGTATTGTGTG  
GTCCTGTATATTCTGTTAAAAAATAAGGACAGAAACCTTCTTTGTGTATGCATGTTTGA  
ATTAAGAAAGTAAGTAAGGAAG

## **FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQGQLLEVGNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVGGIGLFFSFTEILGVWL  
TYRYRNQKDPNPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT  
TGTATTTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCGGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTGTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

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## **FIGURE 17**

AATCCCAAATCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

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## **FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCCTTGTTCAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAACTGCTGTGGGTTCGGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

0570191-103501

## FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACCTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGGAAGCTGGCT  
TCCAGGTCAAGGCTACACTTTCAGTGAACCCCTCCACCTGATTGTGTCTTATGACTGGCTG  
ATCCTCCAAGGTCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGTTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CGGGGCTTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCTTGAGTTGTGAGCAAAAGTTGCCCTGCAGAGGTCAAGTGGCCCG  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTAGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACCTGCTCCTGA  
GGAGGCCCCCTGGGCTCTGCTCCGCGGCCAACCCCATCTTCTGAGGATCCAGGCTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAAACATG  
CAGGATGTGAGAGTCTCTCCTCGGTCACTGCTCATGGAGTTGAGGAAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGCTGCTGCACATATGCATAAGTA  
CTTTTCAAGTTGTCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT  
GTGCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACAAAGAAAAATAATCTGGCCCAAAATGTGAGTTGACTGAGTTTGAGAAA  
CCCCAGCCTAATGAACCCCTAGGTGTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATAT  
TATCTCTTTCCAGCCTCATTAGCTATTCTTACTGACATACCAAGCTTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTTCCACCAT  
ATGAGAGCTGGCAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCGCAAAACACCG  
ACTCTGCTGTTGCCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGTG  
TTGTTTGTAGCCTAA

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSGLVWVAQMMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSSEDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

### **Signal sequence:**

amino acids 1-17

### **Leucine zipper pattern sequence:**

amino acids 12-33

### **Protein kinase C phosphorylation site:**

amino acids 353-355

## FIGURE 21

CCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGCGG  
ATCTTACTGGGCCTGCTACTCTCGGGGCACCTAACAGTGGACACTTATGGCCGTCCTCATCT  
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACTGGCAGACTCTGTATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCAAGTGAACA  
TGGCAGCGGTTATGGCTTCACGGTGCCCGAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACAGGAACCCATC  
AAAGTAGCAACCTTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCTCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAAGTCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCTCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCCGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCAGACCCC  
AATCCTAAGGCCGAGGCGCTTCAAGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCTGTAAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGTAGCCAACTTCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGGCTTCTGCATGGCCCTTCTCCCTGCT  
ACCTCTCTTCTGTGATAGCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGCGCTCAGCTCTGCCAGCTCAGAGGACCAGCACTATATCCAGATCAT  
TTCTCTTTCTTCAAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCTCCACTATAAGTCTAATGTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPIISYIWYKQQTNQ  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

00743.10501

**007-1060-1**

ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVYVGTGLGTHTEIKRVABEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLMTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

# FIGURE 25

GTCTGTTCTTTGCTCTCTCGCGCCAGTCTCTCTCTGTTCTCTCTCAGCCGCTGTGCGGAGGAGACACCCGGA  
 GACCGGGCTGTCAGTTCGCGCGGGCTCTCTCCCGCTCGGGCGGCTCGCCGCTGCGGAGTGTCTGAGCGCCCTAG  
 AGCTCTCTCTGCGGCTCTCTCTCTCGCGCGCGCAGCAGTGCACATGSGGTTGTTGGAGGTAGATGGGCTCCG  
 GCCCGGAGGCGGGGTGATGCGCGCTGGGCGAAGCAGCGCCGATTTCCAGCTCCCGCCGCGCGCCCGGGCG  
 CCCCTCGAGTCCCCGTTTACGCCATGCGGAGCTCTCGAGCAGCAGCAGCGCCCTCGCTCTCTCGCCGCACTC  
 GCGCGCGAGCCACGACCGACGATGATCGCGGGCTCCCTCTCTCTGTTGGATTCTTAGCACCACACGAGCTCAG  
 CCAAGACAGAGGCTCGAATCTCATTTGGCAGATACCGCCATGTTGACCGTGCCACCGGCGAGGTGCTAACTGT  
 GACAGATGTTCAGCAGGAACCTATGTTCTGAGCATTTATCCAAACAAGCTGCGCGTCTGCAGCATTTGCGCT  
 GTGGGACCTTTACCGGATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAAATG  
 ATTGAGAAATTACTTGTCTGCTTTGACTGACCGAGAAATGCACCTTGCCACCTGGCATGTTCCAGTCTAAAGCT  
 ACCTGTGCCCCCATACGTGTGCTCTGTGGGTGGGGTGTGCGGAAGAAAGGAGCAGAGACTGAGGATGTGCGG  
 TGTAAGCATGTGTCTCGGGTACCTTTCTCAGATGTGCCCTCTAGTGTGATGAAATCAAAGCATACACAGACTGT  
 CTGAGTCAGAACCTGGTGGTATCAAGCCGGGAGCAAGGAGAGCAGACAAAGTCTGTGGCAGCTCCCGTCTCT  
 TCCAGCTCCACTCACTCTCCCTGGCACAGCCATCTTTCCAGCCCTGAGCAGCATGGAAACCCATGAAGTCCCT  
 TCTCCACTTATGTTCCCAAAGGATGAACTCAAAGAAATCAAACCTTTCTGCTCTGTTAGACCAAAGTACTG  
 AGTAGCATCCAGGAAGGAGCAGTCCCTGACAAACAAGCTCAGCAAGGGGGAAGAGCGTGAACAAAGACCTC  
 CCAAACCTTCAGGTAGTCAACCAACAGCAGGCGCCCGCCACACAGACACATCTGAAGCTGCTGCGCTCCATGGAG  
 GCCATGGGGCGAGAACTCCAGCAGCCATCAAGGGCCCAAGAGGGGACATCTAGACAGAACCTACACAAG  
 CATTTTGTGATCAATGAGCATTTGCGCTGGATGATGTGCTTTCTGCTGCTGGTGTCTGTGTGATGTGGTG  
 TGCAGTATCCGGAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAGGCA  
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTACTGATTTCTTTGCAATGCCAGTGAG  
 AGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACACAGAGCGGGCTAGCAGCTCTGAGCAGCTTGGACC  
 ATCCGGGGCCCGAGGCGCCCTGCCCCAGCTAATTAGCGCCCTGCGCCAGCAGCGGAGAAACGATGTGTGGAG  
 AAGATTCTGGGCTGTATGGAAGACACCAACCCAGCTGGAAATGACAAACTAGCTCTCCGATGAGCCCGACCGG  
 CTAGGCGAGGCCCCATCCCAAGCCCAAGCGGAAATCTGAGAAATTCGCTCTCTGAGCTGGAGGCTTCCCCA  
 CAGGACAAGAAACAGGGCTTTCTGCTGGATGAGTGGAGCCCTCTCCGCTGATGACTCTACCTCAGCGCGCTCC  
 TCCGCGCTGAGCAGCAACGGTCTTTATTACCAAGAAAGAAAGGACAGTGTGCGGCTAGGTACGCGCTGGAC  
 CCCTGTGACTGTCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCTTGAGGAGCTGCGGGTGTATGAAGAG  
 ATTTCCCGAGCTGAGGACCAACTAGACCGGCTATTCCGAATTTATGGAGTCAAGACCAAGGAGCCAGCCAGACC  
 CTCCTGAGCTCTGTTTATAGCCATCTCTGACCTGCTGTAGAACATAGGATACTGCATCTCGAAATTACTCA  
 ATTTAGTGCAGGGTGGTTTTTAATTTCTCTGTTTCTGATTTTGTGTTGGGGTGTGTGTGTGTGT  
 GT  
 TCTCTCTCTTTTTTTTTTAAATAACTCTTTCTGGGAAGTTGGTTTATAAGCCTTTGGCCAGGTGTAATGTTGTGAA  
 ATACCCACCACTAAAGTTTTTAAAGTTCCATATTTCTCCATTTTGCTCTTATGTATTTTCAAGATTATCTG  
 TGCATTTTAAATTTACTTAACCTACCATAAATGAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
 TTTTAAAGTATAATGGCATCTGTGGAATCTTAAAGCAGTCTTTATGTCTCTTAACATTCACACTACTTTTT  
 AAAAAACAATATTAATACTATTTTATTATTTGTTGCTTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
 CCCCATTGAGTTACTGTAATGCAATTTCACTTTGAGTTATCTTTTAAATATGCTCTGTATGATTCATATTAGT  
 CTGAAGATTTGACACACATATTTGCTGATTGTATGGTTTTACCTGAGACCCGTGTAGAAATGCTTGTATTACTTGTAC  
 TCTCTTTATGTGTAATGCTGCAACTGGAGGCTGGAGAAATGAAATCTCAAGCCATCAGGATTTGCTATTAAAGTGGCT  
 GACAACTGGGCCACCAAGAACTGAACTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTTGCTGCACTTT  
 GGAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAAATTTGCCAGCTTTGCTTTAAAGATGATCTGT  
 TTTTTTATATACATATATCAATAGGTTCAATCTGCTCTCAAGCGCTTGGTCTGCTGGTGGGATTTCTTCAACAAAT  
 ACTTTAAATTAATAATGCTGCAACTGTGAAGAACCTGTCTGATATTTTGGCACTATGCTCCCAATTTACAAGT  
 TACCTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTTGGCTGGAATCCCTTTGTGTGGGTGGGTTTGTG  
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCTCTCAAGTGTACTAATTTATTAATAAATCAGATTGTTGTGTA  
 AAAAAAAA

0978191.103501

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK  
SSRTLKKGRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNGSFITKEKKDVTLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEIIGVKSQEASQTLLEDVSYSHLPDLL

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 350-370

## FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTCCGTGGTGCCATCTACATTTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTGAGAGGTCTGAAATAGTCAC  
CATGGGGGAAAAATGATCCGCTGCTGTTGAAGCCCCCTTCTCATTTCCGATCGCTTTTTGGCC  
TTGATGATTTGAAAAAAGTCTCTGTTGCACCCAGATGCAGATGCTGTTGCTGCAAGATCTCTG  
TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTTCAAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCTGTGCCCAAC  
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAAACCAGAGTGAGCTCGCTGGAGGGGAGTTTC  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGGAGGATGTGCCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT  
GTGGTCATAGAAGGGGTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGCTCTGTGATCAC  
GCCCCGTGTGGATCATCACTGTGTCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCACTTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCCACTCAGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAGGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCTGTCTGAAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCAAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGGGCCCCGTGGTGTGTCAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACCAAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTCACTCCTTCTCGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCCGATCCTCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCTTGGAGCTCTGAGTTCTCGGCACCA  
GTAGCAGGCCCGAAGAGGCCACCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT  
GTTTTTTGTTTTTTTGGAGGTGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCACTGGCGAAA  
TCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA  
GTAGCTGGGACCAAGGTGCCCGCCACCACACCAACTAATTTTTGTATTTTGTAGTAGAGC  
AGGGTTTTCAACATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTT  
CAGCCTCCACAGTGCTGGGATTACAGGCATGGGGCCACACGCGCTAGCCTCAGCTCCTTTTC  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCCAGGCTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAGC  
TGCAAGAGCCACCAAGCCACTCAGAAAAGACGACCAGCCAGAGTGCAGAACTGCAGTC  
ACTGCAGTTTTTCTCTCTAGGACAGAAACCAACCCCTTTTCACTTCCAACTTAT  
TTTCACATGTGGGAGGTAAATCTAGGAATGACTCGTTTAAAGGCCATTTTTCATGATTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTGGATTCCAATAATATGTTTCTTCCCT  
CATTTGCTGCGGTGCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIILILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKV TALHH  
SVYVREGCASGHVVTLQCTACGHRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIITAACHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR  
DVGGIISPSMLCAGYLTGGVDSQCQDGGPLVCQERRLWKLVGATSFSGIGCAEVNKPVGYYT  
RVTSFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

# FIGURE 29

CCCACGCGTCCGTCCTAGTCCCCCGGGCCAACTCGGACAGTTTGGCTCAITTTATTGCAACGGTCAAGGCTGGCTTGT  
 GCCAGAACGGCGCGCGCGCGCGCAGCAGCAGCACAACAGCGGGGGGAACTTTTTTAAAAATGAAAGGCTAGAGA  
 GCTCAGCGGGCGCGCGCGCGCTCGCGAGGGGCTCGGAGCTGACTCGCGAGGCGAGGAAATCCCTCGCGTCGCGA  
 CGCCCGGCCCGCGCTCGCGCGCGCGCTGGGATGGTGACGCGCTCGCGCGGGGGCCGAGAGCTGCTGCACATGAAG  
 GCGCGCGAAGTGGCAGCGCGCGCGCTGCGCGCTGCTCCCGCGCGCGCTCTGCTCTCGCCCTGGCGGGTGTCT  
 GCTCGCGCCCTCGCAGGCGCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCTCTGT  
 TCGGAGTGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTCTGAATATTTCGACT  
 ACAACCGGAAAGCAAGAGACTGATCATAAATCTGGAAAGAAATGAAGGCTCTATTGCGACAGTGTTCACGGAAAC  
 CCACATATCTGCAAGACGGTACTGATGCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
 ACGGGGATATTCTGATTCAGACAGTCACTCAGCAGCTGTTCTGTGCTCAGGGGACTTATTTGTGTTGAAAAATGA  
 AAGCTATGTCTTAGAACCAATGAAAGTGCAACCAACAGATACAACCTCTTCCAGCGAAGAGAGCTGAAAGCGT  
 CGCGGGATCATGTGATCACATCAACAACACCAAACTCGCTGCAAGAAGATGTGTTTCCACCACTCTCAGAC  
 ATGGGCAAGAAAGGCAATAAAGAGAGACCTCAGGGCACTAAGTATGTGGAGCTGGTGTCTGTCAGACAACCG  
 AGAGTTTCAGAGGCAAGGAAAGACTCTGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCAGTTGACAA  
 GTTTTCAGACCACTGAACATTCGGATCGTGTGTTGGTAGGCGTGGAAAGTGTGGAATGACATGGAACAATGCTCTGT  
 AAGTCAGGACCCATTCAACAGCTCCATGAATTTCTGGAATGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA  
 TGACAATGCGCAGCTGTCTGAGTGGGTTTATTTCCAAGGAGCAACCATCGGCATGGCCCCAATCATGAGCATGTG  
 CACGGCAGACCACTGCGGGGAATTTGTCATGGACCATTCAGACAATCCCTTGTGTGAGCGGTGACCTGGCACA  
 TGAGCTGGGCACAATTTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCATTTCCCATGGTGTTCAGCAGTTGTCAGCAGGAAGGACTT  
 GGAGACAGCCCTGGAGAAAGGAATGGGGGTGTGCTGTTAACTCGCGGAAGTCAGGGAGTCTTTTCGGGGCCA  
 GAAAGTGTGGGAACAGATTTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGGAAGTGTATGAATCGCTG  
 CTGCAATGCCACCACCTGTACCCTGAAGCCGAGCGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
 GAAGCCTCGAGGAACAGCGTGCAGGGGACTCCAGCAACTCTGTGACTCCACAGAGTTCTGCACAGGGGCCAGCC  
 CTGCGTCCAGCAGCAATGTGTACCTGACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGTACAAATGGCAT  
 TCCACAGCTCAGCAGCAGTGTGTCAAGCTCTGGGACAGAGTGTCTAAACCTGCCCTGGGATCTGTTTGA  
 GAGAGTCAATTCGAGGTGATCCTTATGGCAACTGTGGCAAGTGTCTGAAAGTGTCTTCTGCCAAATGCGAGAT  
 GAGAGATGCTTAAATGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGCAAGTCATGTCATGCGTTCGTTTTC  
 CATAGAAACAACAACTCCCTCTGACAGCAAGGAGGCGGAGTTCTGTGCGCGGGGACCCACGTGTACTTGGGCGATGA  
 CAGCCCGGACCCAGGGCTGTGCTTGCAGGCAAAAGTGTGCAGATGGAATAATCTGCTGAAATGCTCAATGTCA  
 AATATTATGTCTTTGGGGTTCAAGTGTGCAATGCAAGTGCACCGCGAGAGGGGTGTGCAACACAGGAAGAA  
 CTGCCATCTGAGGGCCCACTGGCACTCCCTCTGTGCAAGTTTGGCTTTGGAGGAAGCAGACAGAGCGGCC  
 CATCCGCAAGCAGAAAGCAGGCGAGGAGCTGCAGAGTCCAACAGGAGCGCGCGCAGGGCAGAGGCGCGTGGG  
 ATCGCAGGAGCAGCTCTACTGCTCACTGACACTCATCTGAACCTCCCATGACATGAGACAGCTGACAGCTG  
 CTGCTGTCAGGAGAGTCAACGCGTCCCAAGGCTCTGTGACTGGCAGCATGACTCTGTGGCTTGGCATCTGT  
 TCCATGCAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCTACACAGGCACTGTGAGAAA  
 CAGTGCAAGGAAGGGCAGCGACTTCTGTGTTGAGCTTCTGCTAAACATGGACATGCTTCACTGCTGCTCTCTGAG  
 AGAGTAGCAGTTTACCCTCTGCGAGGCGCCAGCCCTGCAGCAGGAGGAAGAGGACTCAAAAGTCTGGCTTTTC  
 ACTGAGCTCCAGCAGTGGGGGAGAAGCAAGGTTGGGCGCAGTGTCCCTTTCCCGAGTGACACTCAGCTCT  
 TGGGAGCCCTGATGACTGCTCTGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATATATGAAAT  
 AGCAGGGTTTATGTTTAAATTTATCAGAGACCTGCCACCATCCACTCCCAAGCAAACTGAATGGCAA  
 TGAAACAACCTGGAGAGAAGGTAGGAGAAGGGCGGTGAACCTGCTGCTGTTGCTGTCATGCTGACGCTGACCA  
 AGTACTCAGTGTGAGGTTTTCAGAAAGCCAGGGAACCCAGAGTCAACCACTTCAATTTAAACAAGTAGAA  
 GTTAAAAAGTGAACAATGTAAGAGCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT  
 GAAAT

0978191.13504

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDISK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF  
YRPLNIRIVLVGVEVWMDMKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYPPFMVFSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCNATTCITLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVGCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVSXSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLQGGRIILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRRQCQNISVFGVHECAMQCHGRGVCCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQEPVGSQEHASTASLTII

**Signal peptide:**

amino acids 1-28

**2021** is the 30th Road Safety Week.

TCCCAAGGCTTCTTGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAAAGAAA  
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGGAAGGGCAGGANTTCTCGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCTACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAAGTGTCCCTTTCCCCAGTGCACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

## 09673182

[illegible]

### **FIGURE 33**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLALLLPVQVSSFFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

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# FIGURE 34

GCGCGCGGAGAGCGCGCCAGCCCGCGCGGATGCGCGCGCGCCAGGACGCTCTCCCGCTGCTGGCGCCGGC  
 CGGCGGCCCTGACTCGCTGCTGCTGCTGCTGCTGCGCCATGGCGCGCGCGCGCTGCGCGCGCCCGGGCCAGG  
 AGCGCGCGCGCGCGCGCGCGGAGCGGCGCCCGCGCAGACGCGGAGGACCGGACCGGACCGCAGCAAGCACCC  
 TGTATACGCGCCGACATGTTCAACGACGCGGATCCAGAGCGCGCGGCACCTTCGTGATGTTCTTCGCGCCCTGGTGTG  
 GACACTGCCAGCGCTGCAGCCGACTTGGGAATGACCTGGGAGACAAATACACAGAGCATGGAAGATGCGCAAAGTCT  
 ATGTGGCTAAAGTGGAGCTGACGCGCCACTCCGACGTGTGCTCCGCCAGGGGGTGCAGGGATACCCCACTTAA  
 AGCTTTTCAAGCGCGGCAAGAGCTGTGAAGTACCAGGGTCTCTGGGACTTTCAGACACTGGAAAACTGGATGC  
 TGCAGACACTGAAAGGAGGCGAGTGCACACGAGCGGAAAGTGGAAACGCGCCAGTCCCGCGAGCTCAAGCAAG  
 GGCTGTATGAGCTCTCAGCAAGCACTTTGAGCTGCACGTTGCACAGGCGACGACTTTATCAAGTCTTCTCGCTC  
 CGTGGTGTGGTCACTGCAAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGGCTCTGGGCTTGAACATTCGAAACTG  
 TCAAGATTGGCAAGGTGATTGTACACAGCATATGAACCTGCTCCGGAACACAGGTTCTGGGCTATCCCACTC  
 TTCTCTGGTCCGAGATGGGAAAAAGGTGGATCAGTACAAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG  
 TGGAGTCGACGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCGCCGGTGTGGCAG  
 CTGAGCCCGAGGCTGCACAGGGCACTGTGTTGGCACTCACTGAAAAATACTTCGATGACCCATTGCAGAAAGGAA  
 TAACTCTCATCAAGTTTATGCTCCATGGTGGTGGTCACTGTAAGACTCTGGCTCCTACTTTGGGAGGAACTCTCTA  
 AAAAGGAATTCCTGGTCTGGCGGGGCTCAAGATCGCCGAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA  
 AGTATTCGGTACGAGGCTACCCACGTTATGTCTTTCCGAGGAGGGAAGAAAGTCACTGAGCAGCAGTGGAGGCA  
 GAGACCTTGACTCGTTACACCGCTTTGCTTGGAGCCAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTCAC  
 CTCTCTGCGCCAGCTCCCGCAACCTCGCTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGTGTGGCT  
 GTTCAGAAAGCAGAACTACTAAGCGTGAAGTATCTTCTTTGTGTGTGTGTTTCCAAAGCCAAACACTCTACAG  
 ATTTCTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACATGCTGCTGTTGTAACAACTTTTCACTGGCGATA  
 TATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAATAGCGTTGAGGGAAATGAAA  
 TTGCTGGACTATTTGTGGCTCTGAGTTGAGTGATTTGGTGAAGAAAGCAGTCTCAAGAGCATAGTTTACCTGCG  
 CCAGAGCTCTGTTGCTGTGAATCTTCTGCGCAGTATGACGTTCTCTGATCTGATGAAAGCAGCGTTACTTCTGAC  
 GTGCTCAGTAAAGAAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAATCAGTACTGTTCAAGGGAT  
 CCTCTGCTTTCTCACGGGTGAAGATGCTCTTTAGTTCTCATGTTTAAACAGCCAGCGCCAGCTCAATCTGT  
 TGGATGCTCTTCTTAGAAAGGTTAGCATGGAATTTCCACGAGGCTCAATCTCAGTATCTCATTAACCTATTGA  
 AAGATTCCAGTTGTATTGTCACTGGGGTGACAGAGCCAGACAGGCTTCCGAGGCTGGGTATCCAGGGAGGC  
 TCTGACGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTTCTGATGCTCTTGAAGG  
 CTGTCTATCTTGTCTGCTTCAAGGAGGTGCAGCTCTTAATGTATGAAGAAATGGGATGCTTTGATCTCAAGAC  
 CAAAGACAGATGTCAAGTGGCTGCTGCGCCCTGGTGTGCACGGCTGTGGCAGTGTGATGCCAGTGTCCCTTA  
 ACTCATGCTGCTCTGTGATTAAACACCTCTATCTCCTTGGGAAATAAGCAGATACAGGCTTAAGCTCTAAGATA  
 GATAGGTGTTGTCTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGATCTCAACACTCTTCAACCACCT  
 CCCATACGCAAGGGATGTGGATCTTGGCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACCAAGACCATTTA  
 CTGCTGCTGTGAGGCAGAAATAACAGCAGCATCTCGACAGCTCTGCTCTTAAGGAAATCTTTATTAATCAG  
 TATGGTTACAGATAATTTCTTTTAAAAAAACCACTCTCTAGAGAAGCAGCACTGTCAAGAGCTTGTGATCA  
 CACAACCTCAGCTTTCATCACAGAGTCTTGTATTTCCAAAGAAATCAAGTGGTACAAATTTGTTGTTTACATCAT  
 GATACTTTCTAATAAATCTTTTTTTTTAA

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050707Z FEB 64

><subunit 1 of 1, 432 aa, 1 stop

MPARFGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLTADMFTHGTQSAAHFVMMFFAPWCGHCQRLQPTWNLDGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYPTLKLKFKPQEAVKYQGFPRDQTLNWMQLTLNEEPVTPPEVEPPSAPE  
LKQGLYELSSANFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHVELCSGNQVRGYPTLLWFRDGGKKVDQYKGRDLESREYVESQLQRTETGATETVTPSEA  
FVLAEEPADKGTVLALTENNFDITAEIGITFLKFIYAPWCGHCKTLAPTWEHSSKKEFPGLA  
GVKIAEVDCTABERNISKSYSVRGYPTLLFLRGGKKVSEHSGGRDLDSLRFVLSOAKDEL

amino acids 1-32

## FIGURE 36

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACACGAGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCGATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCCG  
GGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTCTCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA

**DISPATCHED**

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><subunit 1 of 1, 277 aa, 1 stop
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MNGFASLLRRNQFILLVFLQIQSLGLDIDSRPTAEVCATHTISPSPGKDDGEKDPGEEG  
KHGKVGMRMPGKGIKGLGDMGDQGNIGKTGPIGKKGDKEGKGLLGTIPGEKKGAGTVDCGRY  
RKFGVQLDISIARLKTSMKFVNKVIAGIRETEEFYIIVQEEKNYRESLTHCIRIGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIVGNDLEREGQMYSDNTPLQNYSNWNEGEPSPDYGHEDC  
VELMSSGRWNPTECHLTMYFVCFEIKKKK

amino acids 1-25

## FIGURE 38

GGTCTCTATCGAATTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCCTCTCCCTGGAAGGAGAAGTCTCAGCTAGAACACGAGCGGCCCTAGGTTT  
CGGAAGGGAGGATCAGGGATGTTTGCAGCGGCTTGAACACAGCGTGCAGTAGAGGAAGC  
GGGCTCCATGGCTGCCCTCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGAGTTCGCGTGGCTTCCGGCGGACTTGGCCCTTTCGGTTCGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCCGAAGG  
TCCCAGGGGGGCTCGAGCTTGGCTTGGCGCCTCGCGGAACCTGGCCAGCAGCGCGCGCGC  
ACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCCCTACGTGCGCTAGGCTGGGACTGGGACCCGACGCGCGCGACAG  
CGCGCAGGGGAGCGCTGGAGAAGCGAGCGGGCAGCGCCGGAGCGGAGATGCAGCGGCCG  
GAAGCGGCGCGAGTTTGCGGAGGGGACGGTCCGCCAGAGGTGGAGGAGCGCGGCCCT  
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGTGGCCAGAGTTTCTGTGGCTCTG  
GTTCCGGCTGGCCAAAGCGCGCTGCGCACTGCTTGTGCCCCACCGCCCTGCGCGGGGCC  
CCCTGTGCACTGCTCCGCACTGCGCGCGCGCGCGCTGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCGGACTTGGCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGCTGCAGG  
CCCAGGAACCCACCTCTGGAATTAGCGATTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGCTGTACATCTTC  
ACCTCTGGCACCACGGGCTTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCAGTACATTTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG  
AACGTGGCCATAAGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCGGGCCCTTCGAGGTGCTGGAGACATATGGACTGACAGAGGCCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGCGTGCTTCTGGCTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTACCACAGGAGAGCCAAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTTGAATGGCAGCCCTGATTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCACCTTATGCCCG  
GCCCGGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGACGTTCTTGGAC  
CAGGCTGTAGGTGCTTACTGCCCCCTCAAACTGCCCGGTACAGCGCCCTCTGGCAGGAAA  
CCTTCGAATCTGAAGAACTTCCACACTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG  
CCGTTGCAGGTGTACTGGCTGTGAGGATCTTTCTATACAGAAGCTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGCGGCCGACACTCTAGAGTCGACCTGAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCAACTTGTATTATTCAG

0976791-10504

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL  
LLKLHLWLPQLRWLPADLAFVLRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFFSYSEAERESNRAARAFRLALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGFPVPGYLSPPQSITDTCLYIFTSGETTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLGLIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQGG  
LLKDVFRPGDVFFNTGDLVLVCDQGFRLRFHDRGTDTFRWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFFK  
QQKVRMANEGFDPSTLSDPLYVLDDQAVGAYLPLTTARYSALLAGNLRI

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486



## **FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTAWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTEFEFVVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

### **Signal peptide:**

amino acids 1-23

# FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG  
TAGGGACCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTCTTCTCTCACTTCGCCGCTCGTGAGTGTGCGGGAGAGATGGCAAACGCGTAGG  
AAAGGACTGGGAAAAATAGCCCTGGGAAAGTGAGAAAGGTGATCAGGAGGCGCGTCCACTACGCGAGTTTATCTGT  
TCTGATCAGAGCCGAGCGAGCGCTCCACTTCGCACTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCC CGCCCTCCGTACACGACCTCCAGGAGAGTACGCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA  
AAAGTTCTGTCCACTGTGATTCTCAATCCTTGCTTGGTTTCTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTCTCTCGGAGTCCCATTAAAGCACTCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGCAGCTGAGAGGAGAGGAGGATTCTTGCAGGTGGAGAGTCTTCCGCTCGTGTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGCTGCCA  
GGGCTGTGCGGGGCTCCGCTCCGCTCTTCCACAGGCTGTGTCTGCTCGGAAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCTTAGAAGAGGAGG  
AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCAACTTCCACCTCCAGGCCCTCTCA  
TTTTCATCTCTAGCGATGATCAGGATTATGAGATGTGGGTTACCAAGGATCTGAGATTAAAAACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCTTATTGACACCATCCAGGAGTCACT  
TTATTTACTGGAAAGTATCAGATACACCGGACTTCAACATTTCTATCATAAGACCTACCCAAACCACTGTTTAC  
CTCTGGACAATGCCACCTACCTCAGAACTGAAGGAGGTGGATATTCAACGCATATGGTGGGAAATGGCACT  
TGGGTTTTAAACAGAAAAGAAATGCATGCCACCAAGAGAGATTTGATACCTTTTGGTTCCCTTTGGGAAGTG  
GGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATCTCCACAGATGTACACTCAGAGAGTACAGCAAACTTAGCTTCCCAT  
ACCCCAACAAGCCTATATTTTTATATATGCTTCAAGCTGTTTCACTTCCACTGCAAGCTCTTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAGATATGCTGCCATGCTTCTCGCTTAGATGAAGCAA  
TCAACAACGTGACATTTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCACTTACTCTTCAGATAATG  
GTGGCCAGCCTACCGCAGGAGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCTAGCCCACTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCATCACTG  
ACTGGTACCCCACTCTCATTTCACTGTGAAGGACAGATTGATGAGGACATTCACCTAGATGGCTATGATATCT  
GGGAGACATAAGTGGAGGTCTTCGCTCACCCGAGTAGATATTTGCATAACATTGACCCCTATACCAAGGC  
AAAAAATGGCTCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTCAGCACTG  
GAAATGTCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTACAGAACCTGGGACCGAACCG  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGTTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAA  
TGCAGTGCCGCTCAGGTATCCCCCAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATTAAGAGGAAACCAAGAAAAGAACCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAA  
GAAGAAGAAACAGCAAGAACGAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCCTAAGCGTCA  
GGCTGTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCGGCCACACTGAAACCTGCTGCTCAGTG  
CCAAGTGTACTCTCTGCAAGCCACACTTAGAGAGAGTGGAGATTTTATTTCTCTCGCTCTTTGAGAAACGTG  
GTGAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACTGCTTTGAAATATAGGAGGAGAACATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAACACTACCTTTGATAAATTAC

059791 101501

[illegible]

## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296  
><subunit 1 of 1, 515 aa, 1 stop  
><MW: 56885, pI: 6.49, NX(S/T): 5  
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYGLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVG YHGSEIKTPTLDKLA AEGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSII RPTQPNCLPLDNATLPQKLKEVGYSTHVMVGKWHLGFNRKEC  
MPTRRGFDTFFGSLGSGDY YTHYKCDSPGMCGYDL YENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSP LQAPGRYFEHYRSI ININRRRYAAMLSC LDEAINNVTLA  
LKTYGFYNN SII YSSDNGGQPTAGGSNWPLRGSKGT YWEGGIRAVGFVHSPLLKNKGT VCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRS PRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPS ECTGNCLQEILATATGSPLSLSATWDR TGGTMNGSFCQLAKVYGFS  
TSQPTHMRGWYTLGTIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

## FIGURE 44

CGGACCGCTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGCTAGCTGCTACGCGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGACCGGTGCGAGAATTGCTCTGCCCCGAGGCTTGCCTCCCGCTGCTGCTCTCCTGGGTGGCAGGTGGTTTCGGGAACGCGGCCAGTGC AAGGCATCAGGGTTGTTAGCATCGGCACGCTCAGCCTGGGCTGTCTACTATGGAACATAAAGTGGCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGGAGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGGGTGGGACCAAAACAAATGCAGATGCTTTCAGGATACACCGGGAACCTGCAGTCAAGATGTGAATGAGTGTGGAATGAAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGTCTTTGCCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGCCACAGTGCCTGTGTCCATCCTCAGGACTCCGCTGGCCCCAAATGGAAGAGAGCTGTCTAGATATTTGATGAATGTGCCTCTGGTAAAGTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTCCACTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCAAGGGTCTCTCAAGGTAAATGCAAGCAGGGATATAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAAATCTGTGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCACAAAAACAGCATGAAAAAGAAGGCAAAATTAATAATGTTACCCAGAACCCACAGGACTCTACCCCTAAGGTGAACCTTCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACTCTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAAGAGAAGAGAAAGCCCTGAAAGAATGACATAGAGGAGCGAAGCTGCGAGGAGATGTGTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACTGGAACAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCGAGATAATGCTATTTGGCTTCTATATGGCAGTTCCGGCCTTGGCAGGTCAACAAGAAACATTTGGCCGATTGAAACTTCTCCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGTCTTTGATTACCGGCTGGCCGGAGACAAAGTCCGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAGACCACAGTGAAGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAACCTGATGCTACCAAAAGCATCATTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCCAAATCGCAGTGGATGGCTCTTGCTTGTTCAGGCTTATGTCCAGATAGCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGATATTGCATCATAGGACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTGTAAGATGCTTTCTTGATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCTCTCAGTCATTTCTGAACTCTTCCNCATTATATATAAAANTGGAAGNTCAGTTTATCTCCCTCCTCNGTATATCTGATTTGTATANGTANGTGTATGNGCTTCTCTACAAACATTTCTAGAAAATAGAAAAAAGCAGAGAAATGTTAACTGTTTGAAGCTTATGATCTCTTGGAGACTATGACATCAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGCTTTTCATAGCCAAACTGTATATTTAATCTTTGTAATAATAA

## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNSKGVCE  
ATCEPGCKFGECVGNKCRCPGYTGKTCSDVNECGMKPRPCQHRVCNTHGSYKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRCVNTFGSYECKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

## **FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCTCTGAGGGCTGACGCGGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGTGCTGTCCAGCCAGAAGAGTGCAT  
GAGCTGGAAGGGTGAAGAAAGATGCCTAGAGAATGGCAATTAAAGAAAAAGATATACT  
TGTTTTGCCCTTGACCTGACCGACACTGGTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCT  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAAATGATTTGAAAGAAGTTGGATCTCAGAACACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTATTTTAAATC  
TTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTAAATAGATATGACTTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAAAAG  
ATTGCCATGAATCTTGCAAAA

## **FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVVVTGASSGIGEELAYQLSKLGVSLSARRVHELERVKRRCLENGNLKEKDILVPLDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWVISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

# FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG  
 TTGCACTCTTCTACACACTACAGCTATTTGTTAGGTTGCCTGCGGCACACGCTGGGCTCTGTCC  
 TGAATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCTGGATCCTGTTCT  
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
 GTGGCTCAGTTTCCGGAAGGTCGAAGAACCCAGGGCAGGCTAAGAGGCACTGAGCCCTCA  
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCTGTG  
 GACAGCGTGCGCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
 CTGGGTCTCACTGCTGCCCACTGCTTTGAAAAAGGCAGCAGCAACAGAAGTGAATTCCTGGT  
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAGAGGTGGGGGTG  
 GCTGCCCTGCAGTTGCCAGGGCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
 GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
 CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACCAAGCT  
 GCACCAAGCAGACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG  
 GGGTGACGGGCCCTGTGTCAGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
 CACTGGGTTCAAGGCTGAGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCTGT  
 GCTGCTGACCAACACAGCTGCTCAGATTCTGGCTGCAGGCTCGAGTTTCAAGGGGACAGCTT  
 TCCTGGCCCCAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGACCCCTCCCATGCGCCTGGGAGGCCAGGCT  
 GATGCACAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG  
 CTGCCCAGTCTTCAATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACGAGA  
 CCGGAGGAGTGGGGCTGAAGCAGCTCATCTGCATGGAGCCTACACCCACCTGAGGGGGG  
 CTACGACATGGCCCTCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
 TCTGCTGCCCTATCCTGACCACCACTGCCTGATGGGGAGCGCTGGCTGGGTTCTGGGACGG  
 GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGGCCTAG  
 GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCGGGGATGG  
 TGTGTACCAAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCTGTCTGGGGCACCCTGCTG  
 CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
 CCCCAGCCAGGCCGGCGGTCTTCAACCGCGCTCCCTGCCTATGAGGACTGGGTGACAGTTTGG  
 ACTGGCAGGTCTACTTTCGCCGAGGAACCAAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
 AACATAAGCCCAACCAACAGCTGCTGAAGAGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
 AGGCAGGCCAAATGGCATTACTGCCCTGTCTCCCCACCCTGTCTATGTGTGATTCCAGGCAC  
 CAGGGCAGGCCCCAGAAGCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
 CTCCCCACCTGCGAGGACAGGGGTGTCTGTGGACACTCCCAACACCACTCTGCTACCAAGC  
 AGGCGTCTCAGCTTTCCTCTCTTACTCTTTTCTAGATACAATCAGCCAGCCACAGTGTGTTT  
 TGAAAATTTCTTTTTTGGGGGGCAGCAGTTTTCTTTTTTAACTTAAATAAATTGTTAC  
 AAAATAAAA

0370191.101504

## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQ GKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGS DLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLNRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGLACGGALVSEEAVLTAAHCFIGRQAPPEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPGERG  
WVLGRARPGAGISSLQTVPVTTLLGPRACSR LH AAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEF  
GSCLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

## FIGURE 50

CGGGCCGCCCCGGCCCCATTGCGGCGGGCCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCGCGTGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCGAGGGCAGCCTTCCACCACGGGGAG  
CCCAGTGTGACGCGCCTCACAGGAAGATGCTGCGTCGGCGGGGACCCCTGGCATGGGTGT  
GCATGTGGGTGACAGCCTTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCGTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTACAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA  
GCTGTGTGCACAGCTTTGTGTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCG  
GACGAGGGCAGCTTCACTGCTTCTGTGAGCATCCGGGATTTCTGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGAGGGTGTGCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCTTGCGGGTGGTGTGGGTGCGAATGGCACCTACA  
GCTGCTGTGTGCGCAACCCGTGCTGCAGCAGGATGCGCACRGCTCTGTACCATCACAGGG  
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCCTGCGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTCTCCAATGGACATGATTCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCTGCT  
GCCTTATTTACAGTACATACATTCTTTAGGGACACAGTACACTGACCACATCACCACCCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTTCAG  
CTGACTGACCCCTGCGCTTATTTACCAAAGACAGATGCATAGTACCCCGGCTTGTGTTT  
TCCAATGGCCGTGATACACTAGTGATCATGTTTACGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGGCGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTCTCTTT  
CCCTCCTTCTCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCCCCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTCTCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCGCTTCCG  
GATGTCTCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAA  
AAAAAAAAAAAAA

## **FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASRLRLQVRVVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGGQGVPL  
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGEGEGSKTALQPLKHSKSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

## FIGURE 52

TTCTGTGACCCTTGAGAAAAAGAGTTGGTGGTAAATGTGCCACGCTCTTCTAAGAAGGGGGAGTC  
CTGAACCTGTCTGAAGCCCTTGTCGGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCTTGGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACCTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCTGGGCATCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGTC  
TCTGGGCTATGAAAAGAAGGAAAAGGTAATAATCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATATTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTTGGTCTTTGAATAGAAGACTCTTGGACAATTTTTCACTTTCACAG  
ATATGAAGCTTTGTTTTACTTTTCACTTATAAAATTTAAAAATGTTGCAACTGGGAATATACG  
ACGACATGAGACCCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCACATTTGAAAAGCCTTTTGCATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGTTTGTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTCGAATGCTGAAAG  
TTAGAAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGCGGTGGTGTGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCCAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATTAGGTTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCTGTTCTTTAATGGGTAGTCTATAGTATATATACTACAATAACA  
TTGATCATAGAATAAAGTAGTAACCAAGTCTACATTTTCCCATTCTGTCTCATCAAAAAAC  
TGAAGTTAGCTGGGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAAACATGGTGAAACCTTGTCTCTA  
CTAAAAATAACAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAAGTGGCCAAAGTTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

0976191.101501

## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

# FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
 CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA  
 CTAACATCTCAGTCTCTGAAATGACACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
 CTGCCACCCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
 TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGAAACAACTGCTC  
 TGAGGAGATGTTCCCTCAGTTCCGATGAAGATCATTAACCTGAACTGGAGCGGTTTCAAG  
 ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACGTG  
 CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
 CCGTGATTGTGGGTGCCCTCCGTCGGGGGCTTCCGTGGCTGTGGTCACTTTGGTGCTGATGGTG  
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTACTGGGTGGCGGGCC  
 CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCCGCTGTACAGTGACCTGCCTGCTCG  
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCCACTTGGGGCTCCTGAACCCCG  
 ACTTCGTATCTCCACCCTGCACCAAGAGTGACCACTCTCTTCCATCCGAGAAACCTGCCA  
 TGCTCTGGGACGTGTGGGCTTGGGGAGAGGAGAGAAAGGGCTCCCACTGCCAGTCCCTGG  
 GGGGAGGCAGGAGGCACATGTGAGGGTCCCAGAGAGAAGGAGTGGGTGGGCAGGGGTAGA  
 GGAGGGGCGCTGTCACTTGCCAGTGCTTGCTGGCAGTGGCTTTCAGAGAGGACCTGGTGG  
 GGAGGGAGGGCTTCTGTGTGACAGCGCTCCCTCAGGAGGGCTTGGCTTGGCACGGCTG  
 TGCTCCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
 AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGGCCAGGG  
 CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT  
 GCTAGTGGCTCCTTGGGGCTCCTGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCATGTTTCCAGCGGGGACCCACCAACAGAGGCC  
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGTGTGAG  
 GCTCTGCCTTCTCCATGGGGTAACCACTCCGCTGGGCAGGGGAGCCAAAGGCTGGGAAAT  
 GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCACTGAGAACTCTCCAGTT  
 GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG  
 GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCTGTCCCATCTGCGGCCACG  
 CTACTCGCTCCTCTCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
 ACAGTGGCTCAGCGCTGTAATCCCAACACTTTGGGAGGCCAAGCGGGTGGATTACCTCCAT  
 CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATAAGAATTAGCTGGGCGTG  
 GTGGCGTGGCCTGTAATCCAGCTATTTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTATAGTGCCACTGCAATTGAGCCTGGGTGAC  
 ATAGAGAGACTCCATCTCAAAAAA

0978191.101501

## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

## **FIGURE 56**

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAGGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAAGTGCCTCTGAGGAGATGTTCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAAGTCTACATCATGAACCCCC

## **FIGURE 57**

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAAC TGCTACATCATGAACCCCCC

09/24.10504

# FIGURE 58

TGCGGCGACCGCTCGTACACCAATGGCGCCTCCACCTCGCGCCCTACCGTGTGGGGCTGCTCCCGGATGGCCCTCTGT  
TCCCTCTGTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGCGCGGAGCTCACCCCCAGTGGTGTCTGTGCTCC  
CTGGTGATTGGGTAAACAACCTGGAAGCCAGGCTGGACAAGCCGACAGTGGTGCACTACTCTGCTCCAAGAGA  
CCGAAAGCTACTTCACAATCTGGCTGAACTGGAACTGCTGCGCTGTCACTATTGACTGTCTGGATTGACAAATA  
TCAGGCTGGTTTACAAACAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCTCACTGGAGTTCTCTGGACCCGACAAAGCAGCGTGGGTTTCTATTTCACACCATCTGTGGAGA  
GCCTTGTGGGCTGGGGCTACACAGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTTGGCGCGAGCCCCAAATG  
AAAACGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCACTGTATGGGGGCCCGGTGGTGC  
TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCGAGCCGAGGCTGTGAAGGACAAGT  
ATATCCGGGCTCTGCTGTCACTGGGTGCGCCCTGGGGGGCGTGGCCAAAGACCTTGGCGCTCTGGCTTCAAGAG  
ACAACAACCGGATCCCACTCATCGGCCCTTGAAGATCCGGGAGCAGCAGCGTCACTGTCTCCACAGCTGGC  
TGCTGCCCTACAACATACACATGGTCACTGAGAAGTGTCTGTGCAGACACCAACATCAACTACACACTGGCGG  
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGACAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCTCTATGGTACTGGCGTCCCCACACAGACTCCTTCACT  
ATGAGAGCTTCCCTGACCGTGACCCATAAATCTGCTTTGGTGAACGCGATGGTACTGTGAACCTTGAAGATGCC  
TGCACTGCCAGGCTGGCAGAGCGCCAGGAGCACCAAGTGTGCTGCAGGAGCTGCCAGGCAGGCAGCACATCG  
AGATGCTGGCCAAAGCCACACCCCTGGCCCTATCTGAAACGTGTGCTCCTTGGGCCCTGCACTCCTGTGCCACAGGA  
CTCTGTGGCTCGGCCGTGGACCTGCTGTTGGCTCTGGGGCTGTATGGGCCACGCGTTTTCGAAAGTTTGTGA  
CTCACCATTCAGAGCCCGCAGTCTTGGACTGTGAAGCATCTGCCATGGGGAGTGTGTTTGTATCCTTTCTCT  
GTGGCAGTGAAGAGGAAGAAATGAGACTCTAGACTCAAGGGACATGGATGGCAAGATGTGCTGTATGGTGA  
ACTGCTGTACCTTAGACTGTGGCTCCACAGGGTGGACTGGCTGGGCCCTGTGTCACAGTCCCTGGCTGGGGCATG  
TGTCGCCCTATTCTGTGGGCTTTTATACACTTGCTACTGGGCCCTGGCCCGCAGGCTTCTATGAGGGATGTT  
ACTGGGCTGTGCTCTGTACCCAGAGGTCACAGGAGTGGCTCCTGGGCCCTCGGGTGACCTTCCACACACCA  
GCCACAGATAGGCTGCCACTGGTCACTGGGTAGCTAGAGCTGTGCTCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCTGGGCGAGCTTAGTACTCCTGCAGGCAGGGGAGTTTGTGCGCTTCTGTGGTTCCAGGCG  
CCTGGGACATCTCACTCCTACCTCCCTACCAAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG  
CCCCAGTCCCGCAGGCTGTGTTCCAGGGGCTTGAATTCCTCGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTCACCCTGGGACTGTGTTCCAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGCTAACCCACCATCA  
CACTGCCACCCCTGCCCTAGGCTCTCACTAGTACCAAGTGGGTGAGCAGGCGCTGAGGATGGGGCTCCTATCCAC  
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAAACTTGAATGGGACCTTGAGAGAGCCAGGGGTCCCC  
TGAGGCCCCCTAGGGCTTTCTGTCTGCCCGAGGGTCTCCATGGATCTCCCTGTGGCAGGAGCATGGAGGT  
CAGGGCTGCCCTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCGGAGAAAGGGTACAGCCTCTAGGT  
GGGTTTCCCAAAGACGCTTCAAGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGAGCTGGATTTTCTCTGT  
TTCATACATGCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTGT  
GATTCTGGCAATAAAGTACTCTGGATGCTGTAAAAAATAAAAAAAAAAAAAA

## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCCKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVDRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSVSTSWLLPYNYTWSPEKVVFVQTPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVFTPDSEFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365

## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCGAGCGGCGGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCCTGTCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTGGT  
GGTGCAGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTTGTTGGTTTTCTGCTTCCTACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCAACCAGAA  
CGCGGAGACCACCGAGGGCTACAGCGCGCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCGCTGGACTTTCCCATCAGCCCTCCTGGAACTGCCA  
GCCCCCTCTCTTTCACCTGTTCCATCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCCTGTGCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCTCA  
CTCAGTTTGTCTCCCCGTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCGGGT  
GGCCTCTGGGCTGCCTCCCGTGTGTGAGGGCGGGGTGCTGCTCATGGCACTTCCTCCTTG  
CTCCCACCCTGGCAGCAGGGAAGGGCTTTGCCTGACAAACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

## **FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYRNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFILASAFFLVVDAYFPQISNATDRKYLVIIGDLLFSALWTFLWFVGFC  
FLTINQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

# FIGURE 62

GAGCCACCTACCTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
 CCGTGGCCGAGGCCCCCGAGGTGGCTGGCCGGCAGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
 ATGTTTCAAGGCTGTGAGGACTCCAAGAGAAAAGCCCGGGCTACTCTCCGCTGGTGGCTGTTTGTGTGCTG  
 GCGCTGCTGCTGCTGGCTTCCGCGGGGGTGTACTCTGGTATTTCCTAGGGTACAAGGCGGAGGTGATGGTCAAC  
 CAGGTGTACTCAGGCACTGTGGTGTACTCAATCGCACTTCTCCAGGATCTTACCOCGCGGAATCTAGTGCC  
 TTCCGCACTGAAACCGCCAAAGCCAGAGATGCTCAAGGAGCTCATCACCAGCACCOCGCTGGGAATCTTACTAC  
 AACTCCAGCTCGCTATTCTTCTTGGGAGGGGACCCCTCACCTGCTTCTTCTGGTTTCATTCTCCAAATCCCCGAG  
 CACCGCCGGCTGATGCTTGGCCCCGAGGTGGTGCAGGCACTGGTGGGAGGAGCTGCTGCTCACAGTCAACAGC  
 TCGCTGCCGTCCCCACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCCTAGTGATCCTGGAAGCCAGTGTGAAA  
 GACATAGCTGCATGTAATTCACAGCTGGGTGTATCCGCTACAGCTACGTGGGGCCAGGGCCAGGTCTCTCCGGCTG  
 AAGGGGCTGACACACTGGGCTCCAGCTGCTGTGGCACTGTCAGGGGCCCAAGGACCTCATGCTCAAACTCCGG  
 CTGGAGTGGACGCTGGCAGAGTCCCGGACCGACTGGCCATGTATGACGTGGCCGGGGCCCTGGAGAAGAGGCTC  
 ATCACCCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCCGGGGCCATCATGGCGGT  
 GTCTGGAAGAAGGGGCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCTGT  
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGGCTCTCTCAGCACCCCGTACTTCCCAGCTACTAC  
 TCGCCCCAAACCCACTGCTCTGGCACTCAAGGTCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC  
 TATGCACTGAGGAGGCAGAATATGATTGGCGGTGACCAGGGCCAGTGGACGATCAGAACAGGAGGCTGTGT  
 GGCTTGCGCATCCTGCGAGCCCTACCGCGAGAGGATCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCAAC  
 TCCAGATCTCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACAGTCCGACCCCTGCCCTGGA  
 GAGTTCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCCAACGGCCCTGGAT  
 GAGAGAAATGCGTTTGCAGAGCCATTCAGTGCCTAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT  
 GATGGGCAGCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCAAC  
 TTCCAGTGTGAGGACCGGAGCTGCTGAAGAAGCCCAACCCGCAAGTGTGATGGGCGGCCGACTGCAGGGACGGC  
 TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCTATTGTTGGTGGAGCTGTGTCTTCCGAG  
 GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
 TGGGTGATAACAGCTGCCCTGCTTCCAGGAGGACAGCATGGCCCTCCAGCCCGTGTCTGGACCGTGTCTTGGGG  
 AAGGTGTGGCAGCAATCGCCTGGCTGGAGAGGTGCTCTTCAAGGTGAGCCGCTGCTCTCTGCCACCCGTACACAC  
 GAAGAGGACAGCATCTGACTGACGACGCTGCTGAGCTGACACACCCGCTGGTGGCTGGCCGGCCCTGGCG  
 CCGCTGTCTGCTGCCCGCGCCTCCCACTTCTTCGAGGCCCGGCTGCACTGTCTGATTAAGGCTGGGGCCCTTG  
 CCGGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCACTGATCCACAGGCTGTGTCAGGACGAG  
 GCCTATCGCTACAGAGTCAAGCCAGCCATGCTGTGTGCCGCTACCGCAAGGGCAAGAGATGCTGTCAAGGT  
 GACTCAGGTGGTCCCTGGTGTGCAAGGCACTCAGTGGCGCTGTGTTCTGGCGGGCTGGTCAAGCTGGGGCTG  
 GCTGTGGCCGCGCTAACTACTTCCGCGCTACACCCGCTCATCAGGTGTGATCAGCTGGATCAGCAAGTGGTG  
 ACCTGAAGAACTGCCCCCTTGCAAAGCAGGGCCCACTCTTGGACTCAGAGAGCCAGGGCACTGCCAAGCAGG  
 GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGTGGCATCTTGTCTCTGTCC  
 CTGATGTCTGTCCAGTGTGTCAGGAGGATGGAGAAAGTGCAGCAGCTGGGGGTCAAGACGCTCCCTGAGGACC  
 CAGGCCACACCCAGCCCTTGTGCTCCCAATTCTCTCTCCGTCCCTTCTCCACTGTCTGCTTAATGCAAG  
 GCAGTGGCTCAGCAGCAAGATGCTGGTCTCATCTCCGAGGAGTGTCTGAGGTGGCCCACTCTGTACAGAGG  
 CTGTTTGGGCACTTGGCTTCCAGAGACAGATTCCAGCTTCGGAAGCCCTGGTCTTAACTTGGGATCTGGGAAT  
 GGAAGGTGCTCCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGTGGGCTGTGTCACCTGTAAAGCCAA  
 AAGGTGGGAGTCTGACTCCAGGTCCTTGGCCCAACGCTGCTGCTGCTGAGCCCTCAGAGCCCAAGCCCT  
 CACTGGGAGGTGAGCTCAGCTGCCCTTGGAAATAAGCTGCTGATCAAAAAAAAAAAAAAAAAAAAA

## FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YNNSSSVYSFGEGLPTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRLKGPDLHASSCLWHLQGPDLML  
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSPTYFSPSYSPQTHCSWHLTPVSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERI PVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGFEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCQDQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPD CRDGSDEEHCD  
CGLQGPPSSRIVGAVSSEGEWFWQASLQVRGRHICGGALIA DRWVITAAHCFQEDSMASTVL  
WTVFLGKVVQNSRWPGEVSFVKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA  
RSHFFPEFGLHCWITGWGALREGGPISNALQKVDVQLIPQDL CSEAYRYQVTPRMLCAGYRK  
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

### Important features:

#### Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

#### N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### Kringle domains.

amino acids 746-758 and 592-609

#### Homologous region to Kallikrein Light Chain:

amino acids 568-779

#### Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

## **FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACCTATGGCTTGTAACAACAGTCGGACCCCTGCC  
CTGGAGAGTTCTCTGTTCGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAAAAGTGCCTTGACAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGCGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCAAGAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCAACCGGTGGTGCCTCGGCGCGCTGCGCCC  
CGTCTGCCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCGTGCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGTGTTCTTCTGGCGGGCTGGTACAGTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT



## **FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLDKLHKPKATQTEVKPSVRFNLRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL  
PLAHQLYTDVNNTRVVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDQDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNNAKMRNKRNSKMYLKTRAGMPFRGNLQSLCEP

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Lipases, serine active site.**

amino acids 163-172

#### **N-glycosylation sites.**

amino acids 80-83 and 136-139

0970101.101501

**09671** In **J0801**

GAGACGGCTGGCGCGACAGCTGGGCTCGAGCGAAGGGCGGGGCGCGGGCGAGGACCACTCTCCCTCCCTCCGCGC  
 TTCCGCTTGCGCTCCGCTGCTGGAGCGCTGAGAGAGTGAAGACAGCACCGCGCGGCTCGAGGCTGTACAGT  
 CGCGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAAGGTGGCGACAGGCGACAGGCGGCTCG  
 CTGCTGTGGGCGGGGCTGTAGGCGAGGGCGCGCCCGCAGTGGCCGACAGCGGGGCTTTCAGAGACCGGCGCGGAG  
 AGAAGAGTTCGGCGCGGAGCGAGAAACACTTCAAAGTTTGGCGAAAGGACACGCCCTACTCTCCGGGCTGGCG  
 CGCGCTCTCCGCGCCCGCAGGCTCGTACGATCAGGTTGAGGCTGAGGCGCGGCGATCGAGGCCCTCGGGGAGGCGG  
 CACAGGAGAGCTGGGCGCGCGGGCTTCAGGCGCGACCCCATCGGTTAGACACAGAGACTCGGGAGCCCTTCCG  
 GCACCTCTGGACAGCCCGAGGCTGGTTGGGCAACCTCTCTCCCTCTCTCTTGGAGGGCTCTGGCCACTTACGA  
 ACCGAATTTATTTTCAAATCATGCTTTTGAGAGACCCCCAGCACTGCTTTAGAAGTGGAGGCGACTTACAGA  
 GGCCCTCGTGGCGGACAGCGCACCTCCCTCGCCAACTGCACTGCACTGGCTCATCTTGGGACAGAGGAACAGACT  
 TCAACATCAGTTTCAGAAAGTACACTTGGCTCTGGCTCAGAGCGGCTTAAACCCTACGCTCCCTCTCCAGCCAC  
 TGATCTCCCTGTGTAGGAGCACTCCAGCCCTCTCGAGCTGCGCCGGGGGCAACGTCACCATCACTTACAGTATG  
 CTGGGGCGAGAGACCATATGGGCCAGGGCTTCTGCTCTCTCAACAGCAAGATTGGCTGTATGGCTGCGGAGG  
 AGTTTTCAGTGGCTGAACACCGCTGTGTAATCTGCTGCTCGACGCTGTGATGGGGTGTATGCTCTTGGGCAATGGCT  
 CTGATGAGCAGGTTTGCAGCTCAGACCCTTCCCTGGGCTGACCCCAAGCCCGTCCCTCTGCTGCTTGAAGT  
 TCACCTTGGAGAGCTCTATGGGGCTCTTCTCTCTCTCGGTATGATACACACTAGGCTCAGTCTCCACCACCCAGT  
 CTGCCATTGCTGCTGGACCCCATATGAGCCGCGGCTGGCCGTGCGCTTCACAGCCCTGCACTTGGGCTTTG  
 GAGATGCAGTGATGTGTATGATCGGCGCTGGGCGCCCTGAGAGACTCCGCACTATCGGTAGTCTCAACCATTC  
 CAATGAGCAAGGCTGTCACTGTGAGAGACATGTCGGCCAGGCTGTTGTGTCTACCAACAGACTGCTTGGAGCA  
 ATGGCTCGTGCTCTAAATGAGCCATACATGTGGGGGCTATGCTGCTCTGGGACAGACGCTTGGCTTGGGCT  
 CTGGCTGGAGCTGGCGAAGGCTTAGTGAGGCTCTGCTACAGTGAAGCAGCGCTTGGACGCTCATAGGACT  
 GTACTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCCACTGAGACACTTCCCTTGGGGGCTCTGGCAGC  
 TTGGTGCAGGCTGCTCTATGCTGCTGCTGACCGCTGACCCACTACCACTTCTGTGCTGTGGGACAGATGAGA  
 GAGCTGTCTGCGCATTTGCAGCTGGCGAATTTTCGATGCGGGGACAGAAAGTGCGTGTATAGAGACGTGGGTGTGCG  
 ATGAGCAGCGACAGGCTGTGGCGAGCGCATGATGAGTGGGACTGCTCTATGTTTCTGCCCGCAAGGTCATTACCA  
 CTGACGCTATTGCGAGCTTAGTGTGCGGCTGCTCTGGTGTATCGCCCTGGGCTGACGCTCAGGCTCATGACCA  
 TTTCCGACCAAGAGTACAGATCTTGTGCCCTCTCCGAGTGGAGGCTGAGATTGTGACAGCAGGACGCAACCC  
 CTCTCTACGGGCGAGTCACTCCGAGGTCGCGCATCCGCACTGTAGAAGACTTCTTCAAGAGAACTCAATGATTA  
 ACTGAGCTCTGGGACAGCTCGCTCTGTCTGTACAGACTTACGCCAGGATATGACTCCAGAGGCTGGGCGAGGTG  
 CGCGCGTGTCTGACGGGCGGCGCTGTATGCGACGCTTGTAACGAGTCTGCGCGCTGGGGCTGTCTCTCTGAA  
 CCAACACCCGGGCTCGGGGCTCTGAGGACGAGATCCAGGTCACAACTTCTGCTGCTCCCTTGAGGCGCTAGATG  
 GTGGCAGAGTCCAGCGCTGAGGCGGGGACCTGGGTTGGGCAATGTGGGAGCAGGACCCCCATGCCCATCA  
 AGGCTCGGCTCCCATCTGTCTAGACAGCTCCAGGCCCACTACTGTCTGAGGCGCCAGGGCGACCTGCTCAT  
 TGGCCCTAGAGGCACTCATTTGTCTGAGTGGTGGAGGCTCGAGGCTGAGCGCTGTGGCCAGCTGGGGCGCC  
 CAGGACCAACCCGAGACCCCTTGAGCCACCAACAGCACTCGGCGCTGGAAGATGAGAGCTGTGCTATGGT  
 TGGCACTGGTGTGAGCGGGGCTGTGGGTAGCTGAGGACAGAGATTGAGCACTGTCTCATGAGGGGACCTGGGG  
 CTCTACTGAGGCTCTCTCCCTGGGGGCTCATCTCATGATGGGCAACACTTTTGAAGAGTGGGTGAGCTCCCTCC  
 ACCACTTCTTCTCTGCTGGTATTTGAGGACTTTGGTGGGCTCGGTTGAGCCCTATGAGTGTGCTATAAAGT  
 TAAGTGTCTCTCAGGACAGGAGAGGGCTCAAGAGTCTCTCTGTAGCTGGGCAATGGCGACAGACCCGAGTCCCT  
 TCACACCACTCTCTCCCAAGGACACCACTTTGGGTGGCTGTTTAAAGAGTAAAGTTTCTTAGAGGCTCATTA  
 GGTGTGAGACCTCATCTCTTGCCAAACTCATCCCAAAGTGGCTTAAAGCAGGAAATGCCAAATCACTTAGAGA  
 CCTCTGACGCCCAAGGGGAGGATTTGGGCAGAACTGAGTTTGGCATCACAATCTCTCTACAGGCTGGG  
 CTCACAAAGAGGTGCAACAAATGCTCTATTCCATGACTACGGCATTGTCTCAGTAAGTTGAGGTCAAAATAAA  
 GBAATCATGACTCTC

[illegible]

&lt;subunit 1 of 1, 713 aa, 1 stop

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPQLPLISLCEAPSPQLPLGGNVITITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEFPQCLNHRCVSAVQRCDGVDACGDGSDAEGCSSDPFGLTRP  
VPSLPCNVITLEDYFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRILAVRPTALDLGFGDAVH  
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP  
WDRPCGLSGSLGAGEGLGERCYSEAQRCDGSDCADGTDDEEDCPGCPFGHFFCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRCQPGNFRRCDEKCVYETWVCDGQPD CADGSDDEWDCS  
YVLPKRVITA AVIGSLVCGLLLVIALGCTCKLYAIRTOEYSIFAPLSRMEAEIVQQAPPSY  
GQLIAQGAIPVEDFPTEPNPNDNSVLGNLRLSLQLRQDMTPGGGPGARRRQRGLMRRLVR  
RLRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPA REGGAVGGQDGEQAPPLPIKA  
PLPASTEFSAPTTVP EAPGFLPSPLEPSLLSGVVQALRGRLPLSGPPGPTRSPPGHTAV  
LLEADEDVVLVPLAEPGVVWAEAEDEPLLT

Signal peptide:

Transmembrane domain:

### LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

## **FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAACATCGCCCCCTTCGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCGTAACCATATATTGTTATCACTGGATTGAAGTACCGTTATCTTATTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAGAAGTTTGTAAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGF EVT VILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVG GGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

**Important features:**

**Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

## **FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTGCACCTGTGACAGCAGTATGCTGTNTTGCCGAC

0978191-10501

## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCACTGGCTCCTGCGCGCGCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
TGCCTCCGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCCACCCGGGACCCGGGACCCCC  
TGCCGAGCGCCACGCCACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGCG  
GCGCGCCAACTTCTTGGCCATGGTAGACAACCTGCAAGGGGACTCTGGCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCGGTGGCAGGAACCCCGCACTCCTACATAGACAGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACTCCCCAAAGCTTTCTCCATGCAGATGTGTGGAGCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAATCTG  
AAATTGGAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCTGGACAGTGGCACCACGCTGCTGCGCCTGCCCGAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCACG  
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAAATCCTGCCTCAGCTTTACATTACG  
CCATGATGGGGGCGCGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAAT  
GCGCTGGTGTATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA  
GAGGGTGGGCTTCGACAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCTTTCTCAAAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGAATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCTCTCTTGTCTT  
AATCGTCTGTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCTGAGGTGCTCA  
ATGATGAGTCTCTCTGCTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAATCAGCTATTAAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGCTTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTACAC  
TGCTTTTGTATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTA  
AAAAAAACTTCATTCTAA

## **FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFVDVTVKYTGGSWTGFVGEDLVITIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR  
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRSRFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGIFYVIFDRAQKRVGFAASPCA  
ETAGAAVSEISGPPSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLLPFRCL  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

# FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCCTGTGCAGGGCGGATCG  
GCAGCCGCCTTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGAGCCGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCGCCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGACGCGCCGTGG  
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGCGCTGGAGCTGGCGCGCCCGGGGAGCG  
CGCGTGGTGTGCGCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCCTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCTATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCTTTTGCCATGCGCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCCTTGCTGAAGGCATGTGCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGGGGACGTCTTGACTTCAAACGCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAAACAGCTTGAGGCCACTGGCGCTCACTGCTATGCAGCCACC  
CAGGGCCTGTGAACTCGAGAGCTGTTCTTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCTGGGAGGATGCTGAACCCGATGAAGACCCCACTGTGAGGACTC  
AGAGGCCCATCTTCTCTAAGCACCCCCACCTGAGGAGCCACAGTTTCTCAACCTTACC  
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGACCCGAATTGAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCTCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCTTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCAGAGTGAAGGAGGAGGGCCTG  
GGATCTGAACCCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCCTTCGCGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCTCGGAATAAAGCGCGTTGACCGCCAAAA  
AAAAAAAAAAAAAAAAA

## **FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPNSEFLRHVPGWLRPLLR  
PLAWLVLRAPRGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL  
AGLPGGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSPQYPSPQSSPDLSKMTHRIQAKVEP  
EIQLS

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Glycosaminoglycan attachment site.**

amino acids 46-49

#### **Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

097011-10300

# FIGURE 76

GGAGGAGACAGCCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATC**ATG**GGAGGCATGGCTCAG  
 GACTCCCAGCCCCAGATCTAGTACACCCACAGGACCAAGCTGTTCAGGGGCTTGGCCCTGCCAGGATGAGCTGC  
 CACAGCCTCAGGCCAGCCACTCTCCACCATCCGCTGTTGCTGAATGGGACGCCCTTGACATGCTGCCACGATGGCCAG  
 CCACACCACTCTTGGCTGATGGGACCTTCTGCTGCTACAGCCCTCTGCGGGGACATGCCACGATGGCCAG  
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCGACGAAACCGGCTTGGCAGCGGAGTGCAGCAGAGGGCT  
 CGGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGACATGTGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGGCGGCCCTGGGGCCACCCAGAGGCCACAGTCTCATGTGGAAAGATGGGAAACCCCTG  
 GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGTCCCTGCTGATGCGAAGAGCAGAGAGAGTGACGAAAGG  
 ACCTACATGTGTGTGGCCACACAGCGCAGGACATAGGAGAGGCGCGCAGGCCGGGTTTCCATCTCAGGAGGCC  
 CAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAAATTCAGCTGGAAATGTGACACTGTGAACCCGGAT  
 CCTGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCGCCTGCCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCGCAGAGCTTGGAGGCCCTCCACTGGGGCCAAAGACTACGAGTTCAAAGTGAGACCATCTCTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTCCCCAGTGCCCCACCTCAGGAA  
 GTGACTCTAAAGCCTGGCAATGGCATGTCTTTGTGAGCTGGTCCCAACCACTGCTGAAAAACCAATGGCATC  
 ATCCGTGGCTACCAAGGTCTGGAGCCTGGGCAACACATCACTGCCACAGCCAACTGGACTGTAGTTGGTGAGCAG  
 ACCAGCTGGAAATCGCCACCTCATATGCAAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGTGGAGCT  
 GGGAGCCGACAGAGACTTCTGTCTCCTTTTGTAGCAGGCCATGGAGCGAGGCCAACGAACCCAGTGAGCAT  
 GGCTCCCTGGACCTGTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCAATGCCACCTCGGTGTGTCACT  
 TGGCTGCTCTTCTGGGCAACCCGCTGTGTATCCACCGCGGGCGCGAGCTAGGGGTCACTGGGCCAGGTCTG  
 TAGCATATCCAGGTGAGGATGCCATCTTAAACACAGGATGGATCAAGTGACTCCAGTGGTTGGCAGACAGT  
 TCGGCTTACACTCTGGCTCTGGGACCTGAGCAGCAGCAGCCTCAGCAGTCCGTGGGTGGGGCGGATGCCCG  
 GACCCACTAGACTGTGGCTCGCTCTCTGCTCTCTGGGACTCCGAAGGCCCGGGCTGCCCTGTCTCCAGACAC  
 AGCACTTTTATGGCTCCCTTACCTGAGCTGCCCTCCAGTACCCAGCCAGCTCAAGTCCAGTCCAGCT  
 CTGAGGCGGCTCCACCCAGCCTGGCCAGCTCTCCAGCCCTGTTCAGCTACAGACACCTCTGAGCGCGCAGG  
 GACTCTCTCTCTCCCGCTTGTCTGTGCCCTCTGAGGGCTTGGAGGCCAAGAGCCAGCTGAGGATGCCAGT  
 GCCAAGTGTCCCACTGCTCCGGGGCAGCCACTCCTTGAAGCTCCGGCCTGTGGACTTAGAAATAGAGGTTCC  
 AAGAACCTTTCCCAAAGCCAGGAGCTGTGCCCAAGCTCTGGTCTGGCGCCCTGGGACCCGAACCTCTC  
 AGCTCTCTCAAATGAGCTGGTACTGCTCATCTCCCTCCAGCACCTCTTCTCTCATGAACTCCCCAACCTAG  
 AGTCAACAGACCCAGCCTCCGGTGGCACCAAGGCTCCTCTCCATCTCTGCTGCCACAGCCCTCACTCCCATC  
 CTTAGCCCTGCGACTCCCTTAGCCCCCAGGCCCTCTCCCTCTCTGGGCCAGCCAGCTTCCAGTGGCTGTCC  
 AGCTCTCATCTGTCTCTCTGGGGGAGGATCAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
 CTCAGTGAGGGGTGAGGAGACTCCCGAGAACAGCGTCTCTCCATGCCAAGGGCTCCTTCAACCCCCACCACTAT  
 GGGTACATCAGCGTCCCAACAGCCTCAGAGTTTACGGACATGGGACGAGCTGAGGAGAGGGTGGGGGCCAAGGG  
 GGAGTCTTGTCTGTGCCACCTCGGCCCTGCTCACCCTCACCCAGCGAGGCTCCTTAGCAATGGTTGGGG  
 TCAGCTCTTGAGGACAATGCCGCAGCGCCAGAGCCAGCCTTGTGAGTCTCTCGATGCTCTCTCTCGCTGAT  
 GCTCACTTTGGCCGGGCCCTGAGCAGTGGCTGTGGATAGCTTTGGTTTGGTCTAGAGCCCAAGGAGGAGCAGACTG  
 GTCTTTCATAGATGCTCATCACTCTCTCCCCACGGATGAGATCTTCTGACCCCAACCTCTCTCTCGCCCTC  
 TGGAGGTGAGGAGGAGCAGCTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGCTGGGAGGGGGATGCCCTCC  
 TGGCCCTCTGACTCTCAGATCTCTTCCACAGAGAAGTCACTCCACTGTCTGATGCCCAAGGCTGGTGTCTCTCT  
 GTAGATTCTCT**TGA**AGCTGTCTCTGAGACTTCCAGACGGGAATCAGAACCACTCTCTCTGTCACCCACAG  
 ACCTGGGCTGTGGTGTGGGTCTTGGCCTGTGTTTCTCTGAGCTGGGGTCCACTTCCCAAGCCTCTCAGAGAG  
 TTTCTCCCTCCAGATTGTGAACACAAATGAAAAACAAATATAGAGCAAGCTCAGTGGAGCCTCAGGGAGCAAA  
 ACATCATCTCCACTGACTCTTAGCCACTGCTTTCTCTCTGTGCCATCCACTCCACACACAGGTTGTTTGGC  
 CTGAGGAGAGCCCTGCTGCTCTTCCCCACATTGGATCAGAGGAAGTGGAGGAGCAGAGGTGCTCTCT  
 GTGAGGAGCAGCAGTGGCTGTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGGCCCTCTCAGCCTTCACT  
 GGGCCCTCTCTCAGGAAGAGCTCAACTCTCTCCCACTCACCATGGAAAGAAATATATGATGCACTGCCACT  
 AGGCACCTGAGGCCCTACTCTATGCCAAACAAAGGGTTCAAGGCTGGTCTAGCGAGGATGCTGAGGAGAGGGAG  
 TATAGACAGTGGTCAAAAGCACACTCTCGTACTGTTGTCACTAGCTTAGAATTTGATACCATATAAAT  
 GGTAAAAA

0978191.103501

## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404  
<subunit 1 of 1, 985 aa, 1 stop  
<MW: 105336, pI: 6.55, NX(S/T): 7  
MGGMAQDSPPQILVHPQDQLFQGPFGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPFWGHEPEPTVSWWKDGKFLALQPGRHTVSGGSLLMARAEEKSDEGYMCV  
ATNSAGHRESRAARVS IQEPQDYTEPVELLAVRIQLENVTLNLPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGDYEFKVRPSSGRARG  
PDSNVLLRLRLEPKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSSTPARPSQVPAVRRLLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS  
SSNELVTRHLPPAPLPFHETPTQSQQTQPPVAPQAPSSILPAAPIILSPCSPSPQASS  
LSGSPASSRLLSSSSLSLGEDQDSVLTPEEVALCLELSEGETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFLEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPFWPPDSQISSQRSQLHCRMPKAGASFPVDYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

# FIGURE 78

CTCCACGGTGTCCAGCGCCCCAGAAATGCGGCTTCTGGTCTCTGCTATGGGGTGTGCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGTTTCAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGAAGTACTGGTGCGAGAAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATTATGTCAGAAAGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
 ACCTCACCTGTCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTTACTGATCTCTCTGTCTTCTTCCAGGACCTGCTGTCCTCCCTCCCTTCTCCAC  
 CTTCCAGCCTCTGGCTACAACACGCTCTGACGCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCTCACCAGCGACCTCTCTCTCTGACGGGAGCTCCCGCCCCCATGTCAGC  
 TGGACTCCACCTCAGCAGGAGACACAGTCCAGTCTCAGCAGTGGCAGCTCTAAGCCAGG  
 GTGTCCATCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGAGCCTTCTGTGAGC  
 CGCAGGCCCTGATCGCCTTCTGACGCCACCTGCTCTGTGGAGAAAGGAACTCAACAGGCCA  
 CGGAGACACAGAGAACGAGAAGTTCTGGCTCTCAGCTTGACTCGGAGGAAAAGGAAGCC  
 CTTCCAGGCCCTGAGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGGATTCGCGAAAGCTTTCACCTCAGCCTCAGAG  
 TCCAGCTGCCGGACTCAGGGCTCTCCCAACCTCCCCAGGCTCTCTCTTTGATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGAGCCAGAGCCGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACAGGCTGCTGACCCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCTCTGGGC  
 CTCATGCCAGTGTGCGACCCCTGCTTCTTCCACTCCAGACCCCACTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCACGGTCTCTCTGATCAGCTGGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGATCCAGCCCTTCAGGAAGCCT  
 GTGAAAAACGTGATTCTCGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAAATGCCAGTGACTGTGCACTTGTAGTTTGAAGGCGAGTGGGCCCT  
 ATGAACCTGCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACCTCTCACCTGCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCTGCTAAG  
 TCCAGGCCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG  
 TTGCCCTTINCCATTGGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACAGAGTGCAGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAGGGGTGCGGGGTGGTGGGTAAGTA  
 GCACAACCTACTATTTTTTCTTTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGTG  
 TCTGCGCCAGGCTGGAGTGCAGTGGCAGCATCTGCAACTCCGCTCTCTGGGTTCAAGTGATT  
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCTGCTTCTCAGTCTCCAAATTGCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGGCCCTATTTCTTTTAAAGTGAATTAAGAGTTGTTAGTATGCAAACTTGGAAGG  
 ATGGAGGAAAAAGAAAGGAAGAAAAAATGTCACTCACTGCTCACCAGACATCAT  
 TATTTTCGTTTTTGTGTAATCTCTCTTCCACTCTTTTCTTCTTACATAAATTGCGCGTGTCTT  
 TTTACAGAGCAATATCTTGTATATACAACTTGTATCTCGCTTTTCCACCTTATCGTTCC  
 ATCACTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

## **FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRRGGILFSRCS  
GTIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLTLQDAGEYWC GVEKRGPD ESSLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
VISMPLHTSEELGFSKFVSA

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

0978191-101501

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAAGTGCCTGTATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCGCGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTGGTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCAGATCAACAGCCGAGGTGGTGCAGCAACCTCACCCGGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGAAAAAGACATCTCAAGTGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCAGGAATA  
AAGGATGGTTGAACGTGAAA

## **FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMVCSDLLNPMLKDTVICAMKITQEPQGLGY  
WEAWRHHCQKDLTEWVDGPDF

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **N-myristoylation site.**

amino acids 67-72

#### **Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

## FIGURE 82

AGCCGCTGCCCCGGGCCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCGTGCGTTT  
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTGCTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGAATCTCGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCAGTACCAGTTCCGGAACCGCGCTGGAACCTGCTCCACAC  
TCGACTCCTTGCCCGCTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGAGGCGCGCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGCGCTGCAGCAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTAGGCTCCTGTG  
AGGTAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCCGCTGGGTCTCTCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGGGACAGAGGGGCCGACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGTGTCTGTGCTGTGGCCGCGGCTTCACACGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTCTGCTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATTGACCGCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA  
GATACTGGTTGATTTTTTGTCTGGTTTGGTTTGGGTCTCATGTTATTTATTTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAGGCTGGGCGCTTGTGGCT  
GCCACTGACCAAAAGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGCGCTTATGGCAGGGAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTTTAACTCTCCAGCACACA  
TACACATGGAATCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTTCAGGCAAGAAGAGGAGATGAGAGCAAGAGACGACTGAA  
GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCCGGGAAGAGGAACTTAACTACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACAGGGATCCCGGCTGTGCTT  
TGCAGTCATGCCCAGTCACTTTTCACAGCGCTGTTCTCCTCATGAACTGAAAAACACACAC  
ACACACACACACACACACACACACACACACAGGACACACACACACACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCCTTGCAGTCATGCCGAGTCACCTTTCACAGCACTGTTCTCT

[illegible]

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

098313 In soils from 03

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCATCGCCATTGGACACACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGCCCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGTTACCACAGTCTTTTGGGCTGTGATTCTGAGTATCTTATTGTCCAAGGCCCTCCACGGAGCGGCGGGCGCTGTGTGACGGCCACGACCTGTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGGGTGCCCTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGACGCGAGGCGCAGCTGCAGACCACGCGCGCGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCGGGAACTGCGTGAAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACGTCCGCACTAGCTGTTCCGGGCGCTGGAGGCCCTGAGGCTCCAGAACCACTCTCGAGCCGTGCCCCCACTGCTGGGCTGCTCTTCGAGGGTCCCTGCTACTTTTCTCTGTGCGCAAGACGAGGTGGGCGGGCGGCAGGATGCTACGCGCATGCCAGCGCGCAGCTGCTGATCGTTGGGGGCCGTGGATGAGCAGGGCTTCTCTACTCGGAACACGCGTGGCCGTGGTTACTTGGCTGGGCGCTGAGGCTGTGCGCCATCTGGGCAAGGTTTACGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTTCAGCCACTGGAACACGAGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTATGATGCTGCACACGGGGCTGTGGAACGACGCAACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACCTGCTTGACCCCGCCCACTGCCCTGGAGCCGCGCCCATTCAGCAGTATGCGTATCTTGGGGCTGTCACTCCCTGGCTCTCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCTCATCCACCGCTGTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCACTGCCCTGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACCCTCCACTAGCTCCAAAATCCCTGCTCTGCTGCTCCCGGTATATGCCTCCACTCTCTCCTCTAACTCAAGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTCTCGCATTTCCACCAAACTGGAAGCTGTTTTTGACGCTTGAGGAAGCATCAATAATATTTGAGAAATGAAAAAA

## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYISKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTAQLQTTRAEELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTLEFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGRLAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:**

**Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287



100-443886-1

```
><subunit 1 of 1, 331 aa, 1 stop
```

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFKQYPL  
 FRPPAQWSSLLGAAHSSDYSMRKNQYVNSGLRDFAEERGEAWALMKIEAAGEALQSVHEVF  
 SAPAVPSGTGQTSAELEVQRRLSLVSFVVRIVPSDFWFGVDSLDCGDRWREQAALDLYP  
 YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLRLRQSP  
 RAFIIPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGHGRLGTKSRTYRVVQPA  
 NNGSPCELTKEEERASDNCV

Signal peptide:

amino acids 1-26



## **FIGURE 89**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVN RVSQSMKGKSSHDLLKDDPHLSSVPVV  
ESEKDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVA EYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDI PETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQSDTFEIIDPRNPVNKRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

# FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCGTTGCCGGGGCAGAGAGATGCTGCCCCGG  
 CCGGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCTTGTCTGACGGCGTCCG  
 AGCCCTGGCCAGACATGTTCCACAGGGTTCCTCTCGGGTCCGGGACTCTGGGCTCCACCACC  
 GTGGCCGCCGGCGGGACAGCACAGCGGGCGTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGAAGTACTTCACTCCAGCAACTACATCTG  
 CTCCTTCAAGTGGTTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
 GGAGGAACAAATACAGGTGCTTGTACACACCAAGAGGCTCAAGTGGTCAACAAATATGGAAC  
 CCTGCAAGGAAAAAGATGTCATGTGGGGAAGACACCCATCCAAGTCTTTTATAGGAGTCCCCT  
 TCTCCAGACCTCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA  
 GGAATCAGAGATGCTACCACTTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG  
 TGCAGTGGCAGATCTCGGCTCAGTGCAACCTCCGCCCTCCGGGTTCAAGCGAGTCTCTCTG  
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCCTGCAGGAGTCTGCGGGCCAGCTGGCCTCG  
 ATGTACGTGAGCACGCGGGGAACGGTACAAGTGGCTGCGCTTTCAGCGAGGACTGTCTGTACCT  
 GAACGTGTACGCGCGCGCGCGCGCGCGGGGATCCCGAGCTGCCAGTGTATGTTCTGGTTCC  
 CGGGAGGCGCTTATCTGTTGGCGCTGCTTCTTCGTACGAGGCTCTGACTTGGCCGCCCGC  
 GAGAAAGTGGTGTCTGGTGTCTCTGAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA  
 CGACAGCCACGCGCGCGGGAACTGGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC  
 AGGAGAAATCTCGAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTTCGGCCAGTCCGGC  
 GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
 CATTTCACAGAGTGGCACCGCGTTATTACAGACTTTTCATCACTAGTAACCCCACTGAAAGTGG  
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAACT  
 GAACCTTCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
 TGATCCAGATGACCCCTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
 CTAGGTGTCAAACCTGGAATTCAATTGGCTCTTGCCCTTATAATATCAACAAGGAGCAGGT  
 ACCACTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCACTGAAGCTCAAGGAGAGAAGATGGC  
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGTTGGC  
 TATGACGGAAGGAGCCAAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
 TGGACATACCTGGGGACAAGAGTCTTACCCACCCAGTTTAGAACTGCAGGAGACTCCCTGCT  
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGGACCTGCACTGCCCTTTCAGCC  
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
 ACCACCTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTTCAAATCTCT  
 CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGTGCAGCCAGACTGCCACTGC  
 CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGTCAACCTTGTTCCTGTCTGT  
 TCACATTTGGCCTGGAGGCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
 TCTTCTCTCCCAACCACTATTCTCCCGAGGCCACTCCAAGTCTATACACAGGGGTG  
 TCTCTTCAATAAAGAAGTGTGTATAGAAAAA

## FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG  
FGTGLFGSKPATGFTLGGTINTGALHTKRPQVVTKYGTQGGKQMHVGKTPIQVFLGVPFSSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA  
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLACNHNSTQILVNCLRALSGTKVMRVSNMRFQLNFRDPPEEIIWSMSPVVDGVVIPDD  
PLVLLTQGGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD  
IVQDATFVYATLQTAHYHRETFPMGICPAGHATTRMKSTCSWILPQEWA

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Carboxylesterases type-B serine active site.**

amino acids 312-327

#### **Carboxylesterases type-B signature 2.**

amino acids 218-228

#### **N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

## FIGURE 92

GAGAAACAGGCCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT  
GCTGTCTCTCGTCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG  
AGTCAGTGATGGTGCAGGAGGCCCTGTGCATCTCTGTGCCCTGCTCTTTCTCTACCCCCGA  
CAAGCTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC  
CAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC  
GATTCAGCTCACTGGGGATCCCGCCAAAGGGGAACCTGCTCCTTGGTGATCAGAGACGCGCAG  
ATGCAGGATGAGTCACAGTACTTTCTTCGGGTGGAGAGGGAAGCTATGTGACATATAATTT  
CATGAACGATGGGTCTTTCTTAAAGTAACAGTGCTCAGCTTACGCCCCAGACCCAGGACC  
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC  
GTCCGACTCCCGTGTGGCCCTATGCCCCAGAGACCTTGTATCAGCATTTACGTCGACAACAC  
GCCAGCCTTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT  
TCCTGCGGCTCCTCTGTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAG  
AACAGAGTCTCTCTCTGTCCTATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG  
GGTGAAGGCTGGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCGAG  
AGCGAGCCCTGGACCTCTCTGTGCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA  
GCAAACAGGACAGTCTTGAAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA  
AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCAGGCTGAGCTGGACCCAGA  
GGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCCTCGGGTT  
CAAGTGGAGCACAGGAGAGTTCACTGCCACGCTCGGCACCCACTGGGTCTCCAGCACGT  
CTCTCTCAGCCTCTCCGTGCCTATAAGAAGGGACTCATCTCAACGGCATTTCTCAACGGAG  
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG  
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC  
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAGCGGAATCAGA  
AAGCCACACCAAACAGTCTCTCGGACCCTCTCCACCAGGTGCTCCCTCCCAGAAATCAAAG  
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC  
CCCAGAAATCCCAGGAGAGCCAAAGAGGAGTCCATATTGCCACGCTCAACTTCCAGGGCTCA  
GACCCAGGCCCTGAGGCCCGGATGCCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC  
CAATGAGGGTCTCTTAGGCTTTAGGACTTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG  
GTTGAAGATAACAGAGTGCAAAGTTTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCCTGTAATC  
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCTGAGGTGCGGAGTTCGAGACCAGCTC  
GCCAATTTGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG  
CGCCTGTAATCTACTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG  
AGGTTGCAGTGAGCCAAAGATCACACCATTTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA  
TCTCAAAAAAAATCCTTCAAATGGGTGGGTGCTGTAATCCAGCACTTTGGGAGGCTCA  
AGGTGGGTGGATTGCTTGAGCCTCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAACCC  
ATCTCTACAAAAATACAAAAATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCAGCTGT  
CAGACATTTAAACCAGAGCACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC  
TACTGGCTGCATTTCTCAGACAGTGGAGGCATTTAAGTCAAGGATGAGACAGGAGGTCG  
ATCAAGATACAGGTCAATAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAACCCAAACCAA  
TCCCAACAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCTACTGCTACTACTCTCT  
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA  
AAAGGGGGAGGAATGAATAATCCACCCCTTGTGTTAGCAATTAAGCAAGAAATAACCATTA  
GTGGGCAACACGAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTCTCTT  
TACTTTCTTAATAAACTTGCTTTACCTTAAAAAA

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK  
AVTETTTKGAPVATNHQSREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCAENRLGSGQQRALDLSVQYPPENLRVMVSQANRTVLENLNGNTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLPLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESSKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 399-418

#### **N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

### **Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

# FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAC TGTTATTTACTGCTGCGTTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCATCTCATTGTAGAGTGAAGCGTGCTGGGTGTGGAACCAATTT  
TTTGTACCCAGAGGAATGAATACGACTAGTCATCACATCGGCCCACTAAGATCTGATTTAGA  
CAATGGAACAATTTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAAGAGCCAGGTAATAGACATCGCTACTGGAAGGCTGTGGAACCTGTGATCTGA  
GTTTGTCTATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGCTCTCCAGAAGGAACATTAGTTATTCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAAACCAACAGGAGTCATAAGAATATCTTCTAAAAATGGATAGAGAAC  
TGCAAGATGAGTATTTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACCTTTTCTGATGTTAATGACAATAAGCCTATATTTAA  
AGAAAAGTTTATACCGCTTGACTGTCTGTAATCTGCACCCACTGGGACTTCTTAAGGAAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGACTTAAGAGGAT  
GATTGCGAAACATTGTGACATTATTACTAATCATGAACTCAAGAAAGGAATAGTTATATTTAAA  
AAGAAAAGTGGATTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTTAAACCAATC  
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCAGCTTTCAATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTGATTTTGAAGTTTTTTGA  
AGAAAACCCACAGGGATCTTTGTAGGCGTGGTGTCTGCCACAGACCAGACAATGAGAAAT  
CTCCTATCAGGTATTTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC  
ACTACAAGTAACCTACTGGATCGTGAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCTATTGTACTAATAGAAGCTGGTTTTAACCCTCAAGAAGAACTGTCTTC  
TACATCTCCATCTTAATTTGCCGACAAATGGAATCCCGTCACTTACAAGTACAACACCCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTTGCTATTCTCATTTTGCAATTATGATCATA  
TTTGGGTTTTATTTTGGACTTTGGGTTTTAAAACAACGGAGAAAACAGATTCTTATTTCTGA  
GAAAAGTGAAGATTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGGAGAAGAAG  
ATACAGGCGCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATTCGCGGGGACCGAAGACT  
CGGAAAACCAACAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAAATTCATTCTGGAAGGCTCGAAGAAGCTTAATCTGATCCGTGTG  
CCCTCCTTTTGTATTCCTCCAGACCTACGCTTTTGGGGACAGGCTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAATAATTAGG  
CGTTTTTACCATAAAATTTTAAAGTGCTAATGTGTATTTCGAACCCCAATGGTATGCTTAA  
AGAGTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTCTTGATTTCC  
CTGGAGTAATATCTCCATGGTTATTTAAGCTACCTACATCTATGACATGGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTGGAAGTAAAAATAATG  
TAGGAAGATATTTAAAGTAGATGAGAGGACAAAGATGATGCTGATCCCTTATGCGATTATAT  
CATTATTTACTTAGGAAGAGTAAAAATACCAACCGAGAAAATTTAAGGAGCAAAAAATTTG  
CAAGTCAAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTTCTTTAT  
TTAA

09070101.101504

094743-1

><MW: 87002, pI: 4.64, NX(S/T): 8

amino acids 136-146 and 244-254

# 2025

ATTTC AAGGCCAGCCATATTTTNTGTGTAACCAACAACAGGAGTCATAAGAATATTTTNTA  
AAATGGATAGAGAACTGCAAGATGAGATTGGGTAAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGATTAAATTAACCTTTGAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAACTCGCACCCACTGGGA  
NTTNTATAGAGAACATCATGGCATATGATATGCATAGGAGAGATGCAAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGCAACATTGTGACATTATT

# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCGCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGCGCGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCCTCGCGGGG  
CCAGGCCACCTTCGGGAGTCCGGGGTTGCCACCTGCAAACTCTCCGCTTCTGCACCTGCCA  
CCCTTGAGCCAGCGCGGGGCCCGAGCGAGTCA**TGGCCAA**CGCGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCTCTGGGATGGATCGCGGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCTTATGCCCGGCGACAACATCGTGACCGCCAGGCCATTGTACGAGGGGCTGTGGA  
TGTCTCGGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAAGTCTTTGACTCCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGCTGCCTTGATGGTGGTTGGCATCCTCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTGCAAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCCTATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGTCTGTTCTGCTCCCCGAAAAACAACCTCTTACCCAAACCA  
AGGCCCTATCCAAAACTGCACCTTCCAGCGGGAAGAGTACTAGTCA**TGTA**CACAGAGGCCAAAAG  
GAGAAAATCATGTTTGAACAACAAACCGAAAAATGGACATTGAGATATCATTAACATTAAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAAACAAACAAAA  
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCTCA  
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTTGAGTAATCACTCAAAAT  
GGGGGAAGGGGTGCTCTTTAAATATATATAGATATGTATATACATGTATTTTCTATTAAAA  
ATAGACAGTAAAAATCACTACTTCCATTATGTTGATACAGTACTTAAATATCTCTTAAAT  
AGGTAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTCGCTC  
TTATATACATATGTAAACAGTCAAATATCATTTACTCTTCTTATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCTTAATTTACCAAGGATGAATTTTCAATTCTTATGCGTGGCCCTTTT  
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCTGAATCTAACACATTTCATAGCTACATTTTA  
GTTTCTAAAGCCAAAGAAGATTTATTACAAATCAGAACTTTGGAGGCCAAATCTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGTCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTATAGTGTATATATCCCCCTAACT  
ACCTTTTTGTTCCTCATTTAATTGATTTGTTTCCCAAGTGTAATATCATGCGCTTTTA  
TATCTTCCATAAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGTGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTTGAGATAATGATACCTAACAGTTAGAAGAGGTAGTGTGAATATAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATGCTTGTAGTGTCTTTATTGCT  
CAGCTGGCTGAGCACTGAAGAAGTCACTGAACAAAACCTACACAGTACCTTCATGTGATT  
CACTGCTTCTCTCTTACCCTTATTTCCACTGAACAAAACCTACACATACCTTCAT  
GTGGTTCAGTGCCCTTCTCTCTCTACCACTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCCTCTCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGCT  
GACATGTTTGTGCTCTGTTCCATTTTAAACAACTGCTCTTATTTCCAGTCTGTACAGAAGT  
CTATTTTCACTTTGACCAAGATGATGTAATGAAAGGGGTGTGGCAGTGGTGTCTGGAGACTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAAGCAAGGATTTGGCTGCTGA  
GCTTATTGCTTCATCTGAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT  
ACTAAGGGAAGAATTGAGGAATTAACGTGATACGTTTGGTGTTGCTTTTCAATGTTTGA  
AAATAAAAAAATGTTAAG

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 22744, pI: 8.51, NX(S/T): 1  
MANAGLQLLGFI~~L~~AF~~L~~GWIGAI~~V~~STALPQWRIYSYAGDNI~~V~~TAQAMYEGLWMSCVSQSTGQI  
QCKVFDSL~~L~~NLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQE~~F~~YDPMT~~P~~VNARYEFGQALFTGWAAASLCLLGALLCCSC  
PRKTTSYPTPRPYKPPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCAGCCCATGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCTGTCCC

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## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCTTGCCTGTCGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNNTGGCCACCGTTGTNNNTGAAGTGATGAAGTGCTTGAAGACGATGA  
GGTGCAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTCTTCTTGCAAGTCTGGCTA  
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCTATGACCGA

09978191.103501

## FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCAACGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT  
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

**Figure 1**

ATTCTCCCCCTCCTGGATGGATCGCNCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCAGGCCATTACCGAGGGGCTTTGGATGTCNT  
GCNTGTGCGAGAGACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGGATCTCTCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCAATTGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGC AATAGANTNNTTNCNNGNNTCTATGACCCCTATGACCCCAAGTCAATG  
CAGGTACGAATTGTGCTAGGCTCTTTCACCTGGCTGGGCTGCTGCTTCTCTGCTCTGCTG  
GGAGGTGCCCTACTTTGCTGTTCTGCTGCC

## **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNNTTCGNGGNTTCTATGACCCTATGACCCCAAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTCTGTCCCCGAA

0925191.10501

## 0405151 101001

AGCAATGCCCTGCCCCAGTGGAGGATTAAATTCCTATGNTGGGGACAACATTGTGACNCGCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGACACCGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGTCTGAATTGTAGCAGACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAATGTATGA  
AGTGCTTGAAGACGATGAGGTGCGAAGATGAGGATGGCTGTCTATGGGGCGCGATATTT  
CTTNTGCAAGGTCTGGCTATTTTAGTTGACCAAGCATGAGTATGGCAATGGAATNGTTCAAGA  
ATTTTATGACCCCTATACCCCACTGAATGCCAGGATCGAATTTGGTCAGGCTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTCTCTGCGAAC

**FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAAGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTTG

0978191-103604

# FIGURE 106

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGATGAAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACACCTCTTACCCAG

0978191.11601

## **FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACNTGCCITGATGGTGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTCTGCGAA

# FIGURE 108

GCGTGCCGTGAGCTCGCGGGGACCGCGGCCCTCGCCCTCGCCCTCGGCCCTCGGCCCTGACAC  
 CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCCG  
 ACCGGTCCCCGCTTTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
 GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG  
 CAGGTCTGAGCCTCGAGCCGACGACGAGCTCAAATTCGAGGTCCCTTACCAGATGTTGT  
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA  
 CAGCACCACTAGGTACTGTGTAGGCCCAACAGCGGAATCATCGATGCAGGGGCTCAATT  
 AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGTT  
 TATGTTTCAGTCTATGTTTGCCTCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
 CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
 GATAAACCACTGATGTAGAAATAAATAAATTATATCCACAATGCATCAAAGACAGAAAC  
 ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTTCAGAGGCTACGGGAGGAGAACAGCAGTTCAAG  
 GAAGAAGATGGACTCGGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC  
 CCCAACTGGGAAGGAAGAAGCCTTAGCACCCGCTCTTGGCTCTGGTGGTTTTGTCTTTA  
 TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGACAGGATGGTAAATTG  
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
 AATGTATGATGACATCTCACAGGTCTTGCCCTTAAATTACCCCTCCCTGCACACACATACAC  
 AGATACACACACAAAATATAATGTAAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
 ATTGAGGGGAAAAAAGAAATGATCTTTATTAATGACAAGGAAACCATGAGTAATGCCAAT  
 GGCATATTGTAAATGTATTTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
 TCTTAAATGACACCTTCTCTCGCTGTTGGTGTGGCCCTTGGGGAGCTGGAGCCAGCAT  
 GCTGGGGAGTGGGTGAGCTCCACACAGTAGTCCCAAGTGGCCCACTCCCGGCCAGGCTG  
 CTTCCTGTCTTCAAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
 AGCCCAAAGGAATTGCACGTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
 TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
 GCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATA  
 TTTAACTTATTAAATGTATTTTCATCTCATGTTTTCTTATTGTCAACAAGATCAGTTAATGC  
 TGCGTGTCTGTAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
 GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
 GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAATTTCTCAGTAGTG  
 ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
 CCACCTCTCAACATTACTCACACTTCCAGCGCCAGGTCGAAGTCTGAGCTGACCTGACCTCCC  
 TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCGAGGGTTAGAAGCGAGGGG  
 ACCAGCAGTTGTGGGTGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
 TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAGAACCCAGTCTGTTTGA  
 CTATGTAGCATCTTGAAAGAAAAATATAATAAGCCCCAAAAATTAAGAAAA

## **FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHCLKFRGPFDDVVTNLKLGNPIDRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMQLQPFDDYDPNEKSKHKFMVQSMFAPDTSDEAVWKEAKPEDLMDSKLRGVFE  
LPAENDKPHDVEINKIISTTASTKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLMRKTVQSNPISALAPTGGKEGLSTRLLALVVLFFIVGVIIKIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

# FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

007914.12113

## **FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTGGGGAGCTGGAGCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACCTCTGTTGGGTGAACGTGATTGCTGCTGGAGGGCTG

**FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACNCGCTGGTAAATTGGATTGGTGGATCCACCATAATCCATGGGATTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTAATGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

0933131

057053X on video format 101

GGTGGCCCCATTCCCGGCCCAGGCTGCTTTCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACGTGTGCAGCATNAGACGTAC  
TTGTNATAAGTAGAGAGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGT  
TTATTTCAGAGATGTTTAAATGCATATTTAATNTATTTTAAATGTATTTNATNTCATGTTTCTTTA  
TTGTCAACAAGAGTACAGTTACATCTCGTGCCTGCTGAANTNTGTGGGTGAACCTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGTGTCATGTGGAGGGTGGG

## **FIGURE 114**

TGCTTTCGGTGCTCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACGTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTCACTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

**0907161**

AAACCTTTAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCGAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCCANTCCC  
GGCCCAGGCTGCTTTCGTGCTTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGGANTGATGA  
ACAGAGTCAGAAGCCCCAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTcantt  
AAAGGNCCAAGNTAAATTTGTATTGGTTTATGTAGTGAAGTCAAANTGTATTAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTCATNTCATGTTTTCTATTGTGCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

## 099783103501

GGCCCTTGGGGAGCTGGAGCCAGCAGTGCCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CAGCTGGCCCCACTCCCGGCCAGGCTGCTTTCCGTGCTCTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAGGAATTGCAGTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAAATAAATGGC  
AGTGTCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTTATGTAGTGAAGTCAAA  
CTGTTATTCACAGAGATGTTAATGCATAATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC  
TTATTGTCACAAAGAGTACAGTAAATGCTCGCTGCTGAECTCTGTGGGTGAAGTGGTAT  
TGCTGCTGGAGAGCTGTGGGCTCCTCTGTCCTGGAGAGTCTGGTTCATGTGGAGGTGGG

# FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCTCCGGCTCAGGCTGGCTGAGA  
 GGCTCCCAGCTGCAGCGTCCCCGCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
 CTCGGGGACCAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTCTCAGTGCCA  
 TGATCATGGTTTACTGACGCTTGACCTCTGGGTTCAAGCGATCTGTCTGAGTAGTGGGA  
 CTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTTACC  
 CTTGGGTGGACCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
 GGTACCCCGGATTGTGAGTGAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAAGCTCCCACTCCCAGC  
 CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
 AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
 TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTTCAGCATCTTGGACAAA  
 AGGTTCTTAACCAATTTCCCTTTAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
 TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAGAGACTATG  
 TCAAAGGGAGTAAAGGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
 AAACGCTCGAGGTTCTAAGAGCGGACAGGAGAGAAGCTAGTGGTGTGACCAAGAGAGGGTAC  
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAGAAGAAAAAATCTGGCCGGGGTC  
 AGAGGATTGCCGAAGGGAGGCCCTTCTTTCAGTGAGCCGGGTCAAGAATACCCACATTCCG  
 AAGGGCTGGGCAAGGAGGATCGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
 GCTGAAGCGTGCTCAGAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
 TGCTGGTGAATGATCCACTTCTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTAT  
 CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
 GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAAATTTGGAAGC  
 GCAAAATCATTTGCGTCTACTCAGGGCACAGTGGGTGGATGTCCACGGGGTTCAGAGGAC  
 TACAACGTTGCTGTTTCGCATCACTCCCTTAAATACGCCAGATTTGCTCTGGATTACAGG  
 GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
 TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
 GAACTCTGTCAATAGCATTTCACATTTTTCAAATCAGGAGATTTTCGTCCATTAAAAAA  
 TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTTCTTTTA  
 CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT  
 AAACCTTCAAACAGGTATTATAAATAACATGTGACTCTTAAATGGACTTATTTCTCAGGGTCC  
 TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGATTAAATGTGAAATTGCATAGATAAA  
 GGTAGATTGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
 CTTGAGATGGATCCATTAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
 GGGACATTTAGTTTAGTTTTTTTGAAGAAATCAAAATCAGAAAGAAAAGCAAGCAATTATAAA  
 CAAAACTAATAACTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTTAAAAAA  
 TGGGAGAAATAGTTTGTCTATGAAATAAACCTTGTAGAAATAGGGAAGCTGAGACATTT  
 TAAGATCTCAAGTTTTATTAACTAATACTCAAAATATGGACTTTTTCATGTATGCATAGGG  
 AAGCACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTTTTATGCTATACAT  
 TCTATGTATGAGGTCTACATTTTAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT  
 CTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTTCTCTGATTAG  
 TAATTTTAGATATGCTCTTCTTCAAAATGAATAAAATTTATGAATATGA

0978791.10501

## **FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNPFSTAVKLSTGCSGILISQHVLTAAHCVHDGKDYVKGSKKLRV  
GLLKMRNKS GGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCVSVDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

#### **Glycosaminoglycan attachment site.**

amino acids 236-239

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCATTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGAATGCTGCCGTGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCACCAGAAGCAGGTGATTTCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTTATGCCAAATTTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT  
GTGGTTGCACCTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCCTGATCACTT  
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAGAGATACTGAGA  
ATGGCTGGACCACCTCAGCAGATTTTATTGTCAAGATTTCGTAACCTGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGTCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCTCGGTGGGAGGCCACCCATGGACCGCGTGTCTCTCC  
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTCAGTGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGTCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGTCTATA  
AACCACAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGAGGAGGCCCTCGTAAAGTTGTAAGAACACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGA  
ACTAAGTGAATCATCTACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA  
AAAAAAA

## **FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLFLFLALLSSRTARSEEDRDGLWDAGPWSECSRTC GGGASYSRLRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNP CSLKCQ  
AKGTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHLYLETKTLQGTKGENSLSSGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTGCGQLRYRVVLCIDHRGMHTGGCSPKTKPHIKECIVPTPCYKPK  
EKLPEAKLPWFKQAQELEEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACCTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGAC  
AGATGCGAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTCTGTGGGCCCCAGGGTCCAGCGGTGCGCAGAGGCGGGGACCCCGCCCTCAT  
GCACGGGAAGACTGTGTGATCACCGGGGCGAACAGCGGCTTGGGCCGCGCCACGGCCGCGC  
AGCTACTGCGCTGGGAGCGCGGGTGATCATGGGCTGCGGGGACCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGGGCCCGAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTTCGGAGTGAACCA  
TCTGGGCGACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAGTTCAGCTCCAGCA  
GGATTGTGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCAGACTTCCATTTATTT  
GGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGATTGTAAGAGGAAAG  
AATGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTTAGCAAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAATAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTGTGCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHIGHFLLTNLLLGLLKSSAPSR  
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGNTVTVNVLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDES VARKLWDISEVMVGLLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

#### **N-glycosylation site.**

amino acids 212-215 and 239-242

## **FIGURE 123**

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTTGGGATAAGAGAATTTTCAAGAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

09978131.101501

## FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC  
CTTTCCTAACCCAAACCCAGCTAGCCAGTCCCAGCCGCGAGCGCCTGTCCCTGTACAGGAC  
CCAGCGTTACCAATGCATCCTGCCGTCTTCTCTATCCTTACCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAAGGAAGAATT  
TCCAATGAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTTGACATAGCCC  
AGAGATACAGGATAAGCAATACCCAACCTCAAATGTTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTGAGGATCAGTGAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACCTCTTGATCGCAGCAAAAGAA  
ATATCATTTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGATGATGACTGTGCCTTCTTCTGCAATTTGGGGATGTTTCAAACCGAAAG  
ATATAGTGGCGACAACATAATCTACAAACCACGAGGCATTCTGCTCCGATATGGTGTACT  
TGGGAGCTATGACAAATTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGGAGACTTCAAAGATGTATTAATTCCTGGAACCTCAAGCAATTG  
TATTTGACTTACATTCTGGAACCTGCACAGAGAATTCATCATGGACCTGACCCCACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCAGAA  
ACTAGACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG  
AAAAACAGTTTGTGAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA  
TATTTTCATAATTTCTATGTGATTTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVFARVDCQHSDIAQRYRISKYPTLKLFRNGMMMCREYR  
GQRSVKALADYIRQQKSDPIQEIIRDLAETTLDRSKRNIIGYFEQKSDSNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPSSSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

## FIGURE 126

ATTAAGGAAGAATTTCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

0978191.12501

## **FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCAGCCCTTTCCTAACCC  
AACCACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTNCGGANCCAGCGTNACC  
ATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGGTGTCTGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

0973191.101501

## FIGURE 128

CCCCACGCGTCCGATGCGGCTTCACGTTCCGCGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAAATACCTGAATCCCCTTGTA CTCTCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTG CAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGGCTTGTGGAAAGACTG  
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTTGTTTATAGGAAC TTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTATTGTAAGACATTACTTAATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACCTGAATGAGAGAAAATGTATATAACCATCCTGCTGTTCTTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

## **FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Type II transmembrane domain:**

amino acids 11-31

#### **Other transmembrane domain:**

amino acids 57-77 and 123-143

09076491-10301

ATTATAGCATTTTGATAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG  
AATCCCCCTTGTACTCCAGAGTACCTCATCCAGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTAACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGAGGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCTACAACCATCATGAATG CAGAT  
ATTCTAGCATATTTGT CAGAAGGAAGGATGGTGCAAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTGGTGAGCTTTTAGAACAACACACAGAAGAATT  
GGTCCAGTTTAAGTGCTATGCAAAAAGCCACCAATAGGAGGTTCTCTCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

## FIGURE 131

CGGACGCGTGGGGGAAACCCCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCC GCCG  
TGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCAAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCT  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAAC TGAGACAAGAACAAC TTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTAAGATGCCCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT  
TGTCCTCTCGGTGATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAAC TGAAATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTTCTGAAAATTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATTCACCTCCTCATAGAGCTTTTAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

## **FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTALAGSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESEACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHLLFPPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 241-260

#### **N-glycosylation site.**

amino acids 90-93

057347-1-1350

### **FIGURE 133**

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG  
TGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978194.101501

# FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTGAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

0976191.101501

# FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
 GGGGCGCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGGACCGGAGC  
 GTGCGGACTGGCCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG  
 GGGATTCTTTGTTTGGCCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
 AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTTGGATGATTGT  
 ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
 ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT  
 GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
 GTTCTGTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
 AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
 AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
 ATTCACTCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCTGAGCGCTACACTGGTTA  
 CAAGGGACCAGATGCTTGAAAATATGGAATGTATCTACGAAGAAAACGTGTTTTAAGCCAC  
 AGACAATTAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT  
 TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGG  
 CCTACATGCAAGCATTAAATGTGCATTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
 AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTGATGGAATTTTGACTGAA  
 GGAGAAGGTCCAAGAAGGCTTAAGAACTTGATTTTCTCTACTTAATAGAACTAAGGGCTTT  
 ATCCAAAGTGTTACCATTTCTCGAGCGCCAGATTTTCACTCTTTACTGGAAATAAAATTC  
 AGGATGAGGAAAAACAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCCCTTTG  
 CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGAAGCACAAACTAAAGGAGGA  
 CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
 GTCTGTGGGAAAGCTTCAGACTCAGGGTTTGGGCACCTGCTCTGAAGATCTTATTTTCTGAG  
 AAATTGATAGCAAAATATGCCAGAAAGTGACCTAGTTATGAATTCATCTAACGAGACAAGA  
 AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC  
 TCAGGAACCTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
 AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGCTCTTAAGCCAA  
 ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTAAAGTAAACACATTTT  
 AAAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
 GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAACAAAAA  
 AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAQRCFCQVSGYLLDDCTCDVETIDRFNNYRLF  
PRLQKLLSDYFRYYKVNLRPCPFWNDISQCGRRDCAVKPCQSDVDPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP  
RYTYGKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALS KVLPPFFERPDFQLFTGNKIQDEENKMLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGSPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

## **FIGURE 137**

GCTGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTATCCAAGTGTACCATT  
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCCTTTGCATTTTGATGAGAATTC  
TTTTTTTGCTG

0970191.101503

## FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCCTTCGTCACCTACCTGTTCTTGCCCCCTGGTGTTCTCTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGTTGGTGGGC  
GCCCCCTGGGATGGGCCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCACTGGGAAATTTCATCTC  
ATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGCTCTGGAAGGTCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA  
AGGTAGGTAAATGTCAGGGAGTAGTCTTCATGCCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTGTGTGGCAGCTCTGTCTTCAGTTCCTGGGATATGTGCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCTGCCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGTCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCTTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTGAGGAGTTCAGACCCAGCCTGGCCAACATGGTGAACCTCCAT  
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA  
AATAATAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
CTCATGCCGTGAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAAGACCCCATCTCTAAATAAATGTTTAAAAAT

## FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSFPNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGMVS

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

SECRET

CACAGTTCCTCCACCACTACTCNTCCCATTCTCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCGAGGATGGGAGGGAAAGTGAAGAAAAAGGAGAGGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACGATCAGGCATGGAACTCCCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACTTGATGAACATACCCACGCT  
ATTCACAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGTTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCACAATGCCCATGTGCCAAGGGCCTCTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGCTCTGTTAGAGA  
CAGATGGTGTATGG

# FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTTGGGCCGGCTCTAGAACA  
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTTCAAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCTATGTGGTTTTTCT  
ACGCATTGATTTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCGCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTTGGAGA  
AACAGTGATCTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATCAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTTGCCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGCTGCATCTGTGTGAAGGCCCAGA  
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTTGGCTTCATGCTGATCCTTGT  
GGTCTGTCCTGTTCTGCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGGCCCCGTGG  
TGGTCTCTCCAGACACCTTGAAATAAACCAATTCAACCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT  
CTCATAGGTTTGGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCACTCCCTTCGGTCTTAAGTTTTCTCACTGTAAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACCGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG  
TGTTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACCTCAAGCCCAATGCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGTGCAGGCCACTGAAAATGGGATGTGCATGAACCGGAGGATC  
CATGAACACTGTAAAGTGTGTGACAGTGTGTGCACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATCGCAGGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTTGTAAAGTACAGAATTGAGCAATAAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA  
AAAAA

0576151.101501

## **FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSTNMKHLMLWSPVIA  
PGETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
AWSILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHV  
KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVEVQGEAIPVLV  
LALFAFVGFMLILVVVPLFVWKMGRLLQYSCCPVVVLPTLKITNSPQKLISCRREEVD  
ACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

0397649 2.4.10.1

TCTTCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCACTATGGTTTTTCTACGCATTGATTCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTTCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCTCTTGTGGCCTANTGGAGGGGGCGAACCCCTTCCGGCGCAAGG  
GTTTNGCGAACCCCTTGGCGCGCTGGGGTATCTCTTCGAGAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAAGTGGCGCTGGGTGTGAT

## FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGAGGAGGAGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTGGGAACCTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCCTCTTTCTGGGGC  
CTGGTGAATGCAGGCTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCGGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCGCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAATCGCGGTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACCTCTACGGGAATTTAGCGCTGCGCTCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCCT  
CAGTCGCTCCTTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCTACTTTT  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGTAACAGCCGGCCCTGCGAGCCCTTGGCCACAGGGCACTGAGGGG  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCATGGTGCCTGAGACTCCCCTTCGAGGATTGCACCGCCCGCTCCTAAGCCTC  
CCCAACAGGCGAGGGGAGTTACCCCTAAACAAAGCTATTAAAGGACAGAATACTTA

## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITTYQGSLSSTPPCSE  
TVTWTILIDRALNITSLQMHSRLRLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPR  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

**Abstract**

GGGCGTGGTGTCTCGCGCGTCTGGGCTGTACGGGACGAGCAGGAGAGTGGCGCGCCAGCGCTCCGCGCGCGGAGCTCT  
GGTGGTCTCCGCGCCCTCGCTCTCTGCGACTGCTCTCAGAAAGCTGGGGCGGCCACCTCGCGACGATACGAA  
CGAGCTCCCTCCCAACGCCAATCGCAGGTCTAATTTTGGACGCTTTGGCTGCCATTTCTCCAGGTCTGAGGGACG  
CGCAGAGCGCGAGGCTCCGCGTATTCTTGAGTCAAGCAACGCTGGCCCCGAGCGCTCGGTGCTCAGCGCTCT  
GCGAGCGGGCGCTCTCGGTCTCGGGTCTGTTGGAAGGCTCTGGCGGCTGTCAGGAGCGCGCGCTCTCGGTTTGGCT  
CACTCTCTCCGAGGAGCTCTCAAGCTGAGGAGCAAAAGGAGTGGGAGAGCGCTGTCTTGGAAGATTCTCTGGGAA  
ATCTCGAGGTCAATTAATTTGAAAGTGTACCGCGCGGAGTGGTCTCAGATGAACACAGGTGCTTTCTGCGTCA  
GCAATTCAGAGCTGGTGGTGGTCCCAATGCCACTTTATTTGGAGAAATTTGGAAAAATATGGATGAGAGATGGT  
GGTGGTGGGATAGCAAAACGAGGGAAAGAGGCCATCAGACACATGACATCGAGAGTATTTTGGACTTCAT  
AATAAATATCAGAAGTCAGGTGTCTTCCACAGCTCTTATATGGAATATATGACATGGGATGTAGAGCTGGAAGA  
TCTCGAGAATCTCGGGCTGAAGTTGCTGTGGGAACATGAGCATCGAAGCTTGCTTCTCAATCAATTTGAGCAAGT  
TTGGGAGCACATCGGGAGAGATATAGGCCGCCGAGTCTTCAATGACAACTGTGATGATGATGAGGAAGCACTTT  
AGCTACCATATGAATGAATGAACCAATATTTGTCATTCAAGGTGTTCTGGCCCTGTATGTAACATATTATACA  
CAGGCTCTGCGCGCAATAGTAAACAGAAATCGGTTGGCACTTAATTTTGTGTCAATACAGAACTCTGGGGGCG  
ATATGCGGCAAGAGCTGTCACTCTGGTGTGCAATTTACTCCCAAGGGAAACTGGTGGGGCGATGCCCTTACAA  
CATGGGCGCGCTGTTCTGCTTCCGCACTAGTTTGTGAGGGGGCTGTAGAGAAATCTGTGCTCAAGAGAGGG  
TCAGACAGGTATTATCCCCCTCAGAGAGGAGAAACAAATATGAATAGAACGACAGCTCAACAAGTCACTGACCC  
CTGTCTCCGACCAAGTCAAGATAGTATGATAGACAGAAATGAAGTCAATAGGCGACCAAGAAATCTCCCAATTTGTTCT  
TGTGAAGTAAAGATTAAGAGATCAGTGCAGGAAGAACCAACTGCAATAGGTGACGAATGCTCTGGTGGTGTGGAT  
AGTAAAGCTAAAGTTATTTGGCATGTATCATTTGAAGATGCAATCCGACATCTGTAGAGGTGCAATTCATTAATGGT  
ATAATAGACATGATGTTGGTGGGTATCATCATAGACAGGAAGAAAGCATTAATTTCACTCAAGTCCAAATGA  
AATGGTATTCAAACAACTTGGCAATATCACTCTGCTTAATTCCTTCACAGCTCTCAAAGTAAACGATTCAGGCTGT  
ACTTGTGAAAACCACTGTGGAACAGCTCTGTCTCAATCTAATAGGCTCGCTCACTTCCGCAAGAGTATATGCTCT  
CGTAACTGTATGCAAGCAAGTCAAGTATGCTCTGTGTAATTTGGAACCTCGAGTTTCTTGATCTGCTGTCAGGAT  
TGTAGACAGCAGTATCACTCGGAGTGGTCTGCAAACTCAGGTGGTATGTATGTATGATCGCTGTGGACAAAGA  
AGAGCTCATTTGCTCTTTTGCAGATGTGAAATCTCTCAGAAAGTTCTCAAGAACTCTCCAGGAGGAAGGCACT  
AAGCTTGTGCTGTGTGTGAAACTGAACTCTGGAAGGAGCACTAAAGACATTCCAATGCAATATTTCTGA  
ATTTTGTATAAACTGTAACTACTTCTAGACAGATACATCAACTATTTTCAGCCGCCAAAGAGTGGCCAAATGCAT  
TAAATCTGTGATAAACAAAGTCTATAAAATAAAACATGGGACATAGCTTTGGGAAAGATGATAAAATATATGG  
TTTAGAAGAACCTGTGGTTAAATATTGCTATTTTCTTAGACGATTTATTCAGACTTAATATACATGATCATGTT  
GTTCTACGTTTTCATATATATATAGTGGCTTTGTATATGCGCACTAAATAAAGTAATTCAAACATTTGAATGTGAATG  
GCCCTCAGAAATCATCTAGTCACTTTAAATAATATGCACTCTAAATACGAAAGAAACCTTTACATTTCTCCCG  
AGTTCAATGCTATGCAATACAACCTGCAATAATCAATAAATTTTCCACTTAATCAACTCTTAAAGTTTCTTCT  
TGTTAATTTAGGACATATAGAAATATAAATCTGGAATGTCACTTCTTATTTATAATAAACTCTTATATATCT  
CAATTAATCTGTTAAATTTGTTGATCTCTTGGAATGGGCTTAAATAAATATGTAATAAAGTCAGAGTGGTGGT  
ATGAAAACCACTCTGATGATCATAGTAAATATGAGGTTAAGCATGGACGACGAGGCTTTCTATGTATCTGTTA  
AAATGGAGTGCACATATTTTCTTTGTATCTCGGCAATATCTCTCGAGCGCAGGAAGTATATAGCAAAAAGT  
GAACAAAGATGAACATATATTTACATTACCTAGCTCACTGATTTTCTTTTAAATGGTAAATGACCTTGTATATA  
ATATGTCATATCATGATGACTTATAAGTGTATATTTGTTCTATGAAAATGATTTGTGCTTGTATATCAA  
AACTGTGAAATGTTGATTTTGGTAAATTTTTTCTGCTGGTGGATTTACATTAATAATTTTTTCTGCTGTGGTA  
TAACTATTAATTTAATCATGTTTCCAAAATAAAAA

## **FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRTTVLFMARAI PAMVVPNATLLEKLEKYMDEDEGEWWIAKQRGKRAITDNDM  
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGFPVCTHYTQVVMATSNRIGCAINLC  
HNMNIWGQIWP KAVYLV CNYS PKGNWNGHAPYKHGRPCSA CPSPFGGGCRENL CYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDCKGTTCNR  
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI  
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCFRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31

# FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
 CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAAGCCGAGCAGAGCTGGGT  
 GCGGTCTCCGGGCCGCGCTCCGACGGGCCAGCGCCCTCCCCCATGTCCCTGCTCCCACGCCG  
 CGCCCCCTCCGGTTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
 ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAGATCCGCTAC  
 AGCGACGTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
 CATCACCAACAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC  
 AGAGACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAAACGAGAAGCGCAGGGTCTACGAA  
 GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACAGTTGGGAGACTTGTGCAAGGA  
 CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC  
 TTTCTCAGGCATAAGACAAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
 TTTTACATTTTATAGCTGCGTGCAGAAAGGCTTCCAGATGGGAGACCCATCTCTCTGTGCT  
 CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTAA  
 AAAATGCTTTTTTGTATTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA  
 GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTGTCTCCATTCTAGCTTGGGAAGC  
 TTCCGCTTAGAGGTCTGGCGCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
 GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGAAGCAGGAGCAGGTCTCT  
 CTGCATCTGTTCTCTGAGGAACCTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT  
 GGTTAATTTTACACACCTAGGAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
 CTTAAAGAAGGTGTGGGCTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
 TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGCAGAAAAACCTTAGGAGAAAAC  
 TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
 AACCTTCAAAGCATGTTTCTTTCCCTCACACAACAGAACATGCAGTACTAAAGCAATATAT  
 TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCTCTTTTCGAAAGCTAAGAT  
 GACCATGCGCCCTTCTCTGTACATATACCTTTAAGAACGCCCCCTCCACACACTGCCCCC  
 CAGTATATGCCGATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACATTAGCAT  
 TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTGAAATGTAAAA  
 AAAAAAAAAA

## FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

09/8191.101503

# FIGURE 150

GCCCAGGGA CTGCTATGGCTTCCTTTGTTGTTACCCCGGCTCTGCGTCA**ATG**TTAAACTCCAATGTCCTCCTGTG  
 GTTAACTGCTCTTGCATCAAGTTCAACCTTCATTGACAGCCAAAGCAGTATCCAGTTGTCAACACAAATTTATGG  
 CAAAATCCGGGCGCTAAGAACACCGTTTACCAATGAGATCTTGGGTCAGTGGGAGCAGTATCTTAAGGGGTCCCTCTA  
 TGCTCAACCCCACTGGAGAGAGCGGTTTCAAGCCCAAGAACCCCGTCTCTCTGGACTGGCATCCGAAATAC  
 TACTCAGTTTGTCTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACTGTCATGACATGTCTGCCATCTGGTT  
 TACCGCCAAATTTGGATACCTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCGCTTTACTTTAAACATCTACGT  
 GCCACGGAAGATGGAGCCAAACACAAAGAAAAACGCAGATGATATAACGAGTAAATGACCGTGGTGAAGACGAGA  
 TATTCAATGATCAGAAACAGTAAAGAGCCCGTCATGGTCTATATCCATGGGGGACTCTTATCATGGAGGGCAACCGCAA  
 CATGATTGACGCGAGCATTTTGGCAAGCTACGGAACGTCTCATGTCATCACCATTAACTACCGTCTGGGAATCACT  
 AGGGTTTTTAAGTACCGGTGACAGGCGAGCAAAAGGCAACTATGGGCTCTGGATCAGATTCAAGCATCTGCGGTG  
 GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCTC  
 CTGTGTCAAGCTGGGAGTGAACTACCAAGCGGCGCAAGTACACTCGGATATTGGCAGACAAAGTGGCTGCAACCT  
 GCTGGACACCAAGGACATGGTAGAATGCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC  
 GGCCACCTACCAATAGCCTTGGGCGCGTGATCGACGGCGAGCTCATCCAGACGACCCCGAGATCCTGATGGA  
 GCAAGGCGAGTTCTCTCACTACGACATCATGTGGGCGTCAACCAAGGGGAAGGCGCTGAAGTTCTGTTGACGGCAT  
 CTGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACTTCTGTGGAACACCTTTACGG  
 CTACCTTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCTATGTACACAGACTGGGCGGATAAGGAAAAACCC  
 GGAGACGCGGCGGAAAACCTGGTGGCTCTCTTTACTGACACAGTGGGTGGCCCCCGCGTGGCGCGGACCT  
 GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCTTCTATCATCTGCAAGGCGAAATGAAGCCAGCTG  
 GCAGGATTGGCCCATGGTGTAGAGGTCCCTATGCTTCTGGCATCCCCATGATCGGTGCCACGAGCTCTTCAG  
 TTGTAACCTTTTCAAGAACGACGTCTGCTCAGCGCGGTGGTCTGACCTCATGACCTCTGTCGCAAACTTTGCAAAACTGG  
 TGATCCAAATCAACCAAGTTCTTCCAGGATACCAAGTTCTATTCAACAAAAACCAACCGCTTTGAAGAAGTGGCGCTG  
 GTCCAGATATAATCCCAAGACACGCTCTATCTGCAATTTGGCTTGAACCCAGAGTGAGAGATCACTACGGGCG  
 AACGAAAGTGGCTTTCTGTGTGAAGTCTGTCTCTCATTTGTCACAACTTGAACGAGATATTCAGATGTGTTTCAAC  
 AACCAACAAAGTTCTCTCACACGACATGACATCATTTCCCTATGGCAACCCGCGCTCTCCGCGAAGATATGGCC  
 AACCAACAAAGCCCGCAGCAATCACTCTGCGCAACAACTCCAAACACTCTAAGGACCTCTACAAACAGGCGCTGA  
 GGACCAACTGTCTCTTGAAGAACAAACGAGATTTATCCACGAATTAAGTGTCACTTGCCTGCGGCGCTG  
 GCTCTCTTCTTCAACTCTTAGCTTTTGGCGCGCTGATCAACAAAAAGGACAGAGGCGCCATGAGACTCACAG  
 GCGCCCGAGTCCCGAGAGAAACACCAAAATGATATGCTCATACAGAACGAGAGAGATCATGTCTCTGTCAGAT  
 GAAGCAGCTGGAACACGATCACGAGTGTGAGTCTGTCAGGCGACAGGACACTGAGGCTCACTGCGCGCGCAGAG  
 CTACACCTCAGCGTGGCGCGTGGCCAGATGACATCCCACTTATGACGCAAAACACCATCACCATGATTCCAAA  
 CACACTGACGGGATGCGACCTTTGCACTTTTAAACCTTCAAGTGAGGACAAAACAGTACAAATTTACCCCA  
 CGGACATTCACCACTAGAGTAT**AG**CTTTGCCCATTATTCCTTCTATCCCTCTGCCCCTACCGCTCAGCAACT  
 AGAAGAGGGGAAGAAAGAGAGAAAGGAGAGAGAGAAAGAAAGTCTCAGACCAAGGAATGTTTTTGTCCCACT  
 GACTTAAGACAAAATGCAAAAGGCGAGTCACTCCATCCGCGCAGACCTTATCGTTGGTGTTTTCCAGTATTAC  
 AAGATCAACTCTGACCCCTGGAATGTGAGAAGTACACATTTCTGTTAAATAAATGCTTTAAGATCTTACCA  
 CTCCAATCAATGTTTAGTGTGATAGGACATCAACATTTCAAGGCGCGGGTGTTCACAGCTCATGGAAGCAGCT  
 GACACTCTGAAACTCAGCCAAGGACCTTGATATTTTTTAATTCAATGGAAGGTTTAAACATTTCTTCTGTG  
 CACACAAATGGATGGCTCTCTTAAATGGAAGAAAGAGTCAATGAGATTTTGGCCAGCACATGGAGCTGTAATCCAG  
 AGAGAAGGAACGTGAAAAATTTAGTATTAAGAAAGTGGACTGTCAGCGAAATCTGTACGTTCTGTGCAAGAG  
 GTGTTTTCGACCGCTGAACATATATTAAAGAGACTTTGT

## FIGURE 151

MLNSNVLLWLTLALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFQPEPPSSWTGIRNNTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN  
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVCNML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHQSEMKP SWADSAHGDEVYV  
FGIPMIGPTELFSCNFSKNDVMSAVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIPQYVSTTTKVPPDMS  
FPYGTRRSPAKIWPPTTKRPAITPANNPKHSDPHKTGPEDTTVL IETKRDYSTE LSVTI  
AVG ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHD  
HECE SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITIMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

# FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGCGGGTCAAACGTTTCGAGTACTTGAACCGGAGCACTCGCTGTCTGAAGCC  
CTACCGGGTGTGGGCACAGGCAGTTCTCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTCCTTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGCGGCCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTCGGTGATTCGCTACGTCAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCTGCC  
CCGCGCTACTACTTCTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCTTGAAGTTGTTTGAAGTACAGTGGAGAGAACCCAGAGAGGAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGCAGCTCCACTGCCGCC  
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTTCCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCTCTCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCACCTG  
GCCTGAGCATGCAGCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTGGGGACATATATTCTG  
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTGTTGTGTCATGGGACATCTAATCT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCTTTCCTGCACTGCT  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTGTGATGCCAAAATCACAGAAC  
AGAATTTCACTAGCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTGT  
AATCCACAAAGAATTAATAACTGGTAACACACAGGCTTTCTGACCATCCATTCTGTTGGGT  
TTGCATTTGACCCAAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAACACAGGATGGAACCT  
TCTTCCCTGCCCTTACCTTCCCTTCACTCCATTTCATGTCCTCTCTGTGTCAACCTGAGCTG  
GGAAAGGCATTTGGATGCTCTCTGTGGGGCTGGGGCTGCAGAACACCTGCGTTTCACT  
TGGCCTTCATTAGTGTGGCCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGGAAGCATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCACTCCAGGTTTGATCAAAACCAAAAGCAACATTTGTCTGTG  
GTCTGACCATGTGGAGATGTTTCTGGAAGTGTCTAGAGCCTGCTTAGCTGCATGTTTGTAGT  
TACGATTTTGGAAATCCCACTTTGAGTGTGAAAGTGTAAAGGAGCTTTCTTCTTACACCTT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCTCGGAAGAGTT  
CACTGTCACTGAGCAGCAGCAGCTGAGTGTGGCTCTGTCAACCTTATTCCTGCTTCACTTA  
TTTGACAAGGGGTTACATGCTGCTCACTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCTTGAAGTCTGAGTCCCTCCTATGAAGCCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCAGTGGAAACCAAAAAAAGGAGGCGCGCGACTCTAGAGTCTG

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPIGSWQQWRRCLSARDGSRMLLLLLLLGSGQGQPQQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEHGQKKK  
LHGDGLAIWYTKDRMQPGPVFGNMDKFGVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFPLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

### **Signal sequence:**

amino acids 1-38

### **Transmembrane domain:**

amino acids 310-329

097031-10303

09701010

CCGAGACGGGCGCGCAGCTCCGAGAGTCGGGGCGGGCCGGGACCATGGGCGTGAGTGCAAATTAAGGATCAGTCTCT  
CTGATGGTGGGTGGTTAACTCAGTCGGGACATCCAGAAATTCATGAAGAAATCAGTTGTCTTCATTCAGAATA  
TGGGGTCTGGCTCAGAATTCGCTCAGCGTGGTGAAAATCTGTTTTCTAGAGAAGGTTTTAATTAATGCTCGACGCT  
GACATCTTCCCGATTTTGAGTGGAACCATGAGAGAAATAAGATAATCTTAATATGCTTTTCGCGAACCGCTCTCT  
TGCTGCTGCTGGCCCTGGCTGGCTGGCTGGCTTTGTAGCGTCAGCGTCAGGTTCTTCCACTGTACCCGGTGT  
CGACTCTCTAAGAATGGAATGAGTACAGAGTGGAGAAAGAGTCTGACCCGACCTGTGACGAGCGCCCTGTGGA  
CAGACCCGTTTATGAAGCTCTTTTGTATGCAACATCCGAGTGTGGCCGAGCGAGCATGGAAGGCTCATGCC  
CGCATCATTTTAGAGCTGGTCTCAGTGCATGTGTTGCTTCGCCACGGAGACAGTGCACCATGTATGATCTTCCCA  
AAACAAGCGCCAGAAATGACTGCATCTGTGTGGCTACAGAAAACCGTATCACCCAAATCGGAAGCTTCCTCA  
TTAGTCAGATGTCAAAGGATCCGAGCGCTCTTTGAAAGCGGCTGAACTCGCTTCCTTTACCCAAATCAACC  
CATTTGTGACATGGAGAGGAGCTCACACAGCAGGTTGTGCAGATTTTGAGAACGCTGAGCTGTGAGGATTA  
TCTATCTAAGAAACAAACAACTGCTGCCAATAGATTTGGTGTGCAGACAGCTCTTGTTATGAGACACCTGGGAAA  
CGCGGACCTCAAAAGTGGGCTGGCTCTGTTTATGGCTTTCTCCAGATTTTGACTGGAAAGAAATTTATTTACA  
GGCCAGCGTCAAGTGTGCGCTGTCTGCTCTGGAAGTGTCTATCGGCGGTTAAGAAACATGATTTGGAAAGGAGC  
AGCGTCTCGTAGCTCTCTAGCTTTGAAAACAGCCAGCTGGGAGAGACATCCGGGAGATGGCCAGATGTGG  
ATGTGCCCAACAGCAGCTTTAGAGCTGCCAACCCATAGACTCCATGCTTCGCACTCTGCCACATCTGCACTGT  
TCCCTGTACAGAAATGTGCTGTGTGTGATGTGAGCAGCTCAAGGTATTCAGAACCATCAGATCGAGGTGAAA  
GGGAAATGACGGGAGAGAAATGTACTTCGGGTATTTCTCTGGTGGCCACCCCATCTGACCAACCAACTCG  
CGCGATGACGAGCTGCCACGGGAGGAGAAAGAAAGCTTTTGCCCTTACTCTGCTCATGATGTCTACTCTGT  
CACCATTCTCAGTGGCTTGGGCGTTTCAGAAAGAGTGTCCCAAGGTGTGACGAGCGGTGATCTTTGAGCTTT  
GCCAAGACAGAGAAAGCCCACTGAAATTCGCTCCGATTCTTTACAAATGGCGTGCATGTACATTTCCAGCCT  
TTCTTGGCCAGGACCCACCAAGCGCTTCCCAAGCCCATGTGCCCGCTTGAAAATCTGGTCCGTTTGTGAAA  
GGACATCTTTAGCCCTGGTGGCTGGTGGTCAAAATTTATTTATGATGATGTACAGGAGAGGATTTCAAAGG  
TATGCAGTACAGCAGTATAGAAATCATGCCAATACAGAGCATAGGAAAGGTCACCTTTAGTTTGTCTGTATC  
TAAGGCTAGAAGATTATGCTTTTAAAGCTAAATATTGTTTGGGAAACACAGATGTGGGTTGGTGAACAT  
AAGCACAATCTGTCAAATGTGGTACGTAAGTTCTGTGTGACAAAATGGCCAGTTTCACAGAGGAATAGAAGTACTT  
TATCATGCGCAGATCTCGCTTAGAATGCGAATAATATGATCTCAGACCTGAAGTTGCCAATCCAAGTTGTGCAC  
TTCTTGGCCTGGCCCAATGTACTATGATGTGAACACAGTACACCTCAACCAAATTTTTPAATCTTAGACATTT  
TTACTTTGCTCTTTGTAAGAAATTTCTTGAAGTATTCTTCAAATTAAGGTGGCAAACTTTTCTGTGAAGGG  
CGAGATTTGAAATATTTAGACTGTGTGACGAAAAGGCCACATACATCTCTGTACATAACTCACTCTGTCT  
TTCTGAAGCAGGAAAGACCCACAGCAGTATAGTAAAGGAATATGTGTAGTCTGGGTTCCAGGCCACAGAAAC  
GATGTTGACAGATCTTGGCCCTGGGCTGTATTTGCTGACCCCTCATCTAAAAATAGGCTATCTACATCATG  
ACTTCCAGCATTTTGAGAACAGTGTGAATACCAAGAAATTTCAATGTGCTACTCTCTGTTGAGTACAGAA  
CAGAATTTGGTCTGTATCTGACATGAGAACAAACTGAGGTTTAAATAAACATGAATAGAAATGAATACAGAA  
AACTGATTAGAGAATAATCTGATGTTTATGATGATTGTGGTACAGATGATTTTAAAGTATTTTAAATATTTGT  
CTGCTGTATCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTAGATTTTATATAGTTTCTAGAAATAAT  
TTCTAAGACAGATTTAGATGACTCTTATCTGTAGTAAATATCAATTTGCTGTACTCTCTGGTGGTTAGAG  
GAGGCTAGAAGATGATTCAGGCATCTTCTTCCATAAGAACAAATTAATGGCTCATCCCTTGCACAGGCTGTAGA  
ACTGGAATTTCTTTAAACCAATTTTACATGATTTCAAATGGTAAATTCGATGATTTTAAATCGGTTTGTGA  
AGAACTTTGCTATTAGGATGTTTACAGATCTTTTAAAGGTGTTTATATATTAGAGCAATATATTTACATCTG  
TGATTTCTGAACTAAATGGTGTCTAAATCAGAAATGGAAGTGAAGTGAGATTTCTGTGTGATCCGGCATCC  
AACTTTTCTCTTTGTTTTTGTCCAGTGTGCAATTTGAAATGTGCTTTTAAATAAATTTTGAAGATTA

## **FIGURE 155**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLALALAALAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDYRPLYVIPTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQGTGVVQHLQNGQLLRDIYLK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSPFC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPPSEHSVRI LYNGVDVTFHTSF  
CQDHHKRS PKMCPLENLVR FVKRDMFVALGSGGTNYDACHREGF

**Signal sequence:**

amino acids 1-18

# FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGGAATACGGTAGATTTCATCCCCCTTTGAAGAACAGTACTGTGGGA  
 GCTATTTTAAGAGATAAAAAAGGAATATCCTTTCTGGGAGTTCAGAGTTGTGCAGTAATTGGTTAGGACTCTGAGC  
 GCCCGTGTTCACCAATCTGGGAGAGAGAAAGCGGAGATCTGCTCGCCTTGCAACGCCCTGAGCAACAGCAGAT  
 AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACCAACGGAGGAGCTTGACTTCCCACTGTCCCATTCTAT  
 GGGCGAAGGAATGCTCTGACTTCAGTGGTTAAGGGCAGAAATGAAATAATTCTCGAGGAGAGATAGAAATGAT  
 TCCTGCGCGACTGCAACGGGACTACAAAGGGCTTGTCTGTCTGGGAATCCTCTGGGAGCTCTGTGGGAGACCGG  
 ATGCAACCCAGATACGCTATTCACTTCGCGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
 GGGGCTGGAGCTCCCGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACCGAGCTTTTCGCCCT  
 GAATCCGCGCAGCGGAGCTTTGTTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGCCATCAAGTG  
 TCAATTAAATCTAGACATTTGTATGGAGGATAAAGTGAAATAATATGGAGTAGAAGTAGAAGTAAGGACATTAA  
 CGACAATGCGCCTTACTTTGTGAAAGTGAATTAGAAAATAAAATAGTGAAAAATGCAGCCACTGAGATCGCGTT  
 CCTCTACCCACGCGCTGGGATCCGGATATCGGAAGAAGTCTCTGCAGAGCTACGAGCTCAGCCCCGAACACTCA  
 CTTCTCCCTCATCGTGAAAAATGGAGCGCAGCGGTAGTAAGTACCCGGAATTTGGTGTGAAACGCGCCCTGGACCG  
 CGAAGAAAAGGCTGCTCACACCTGGTCTTTACGGCTCCGACGGGGCGCACCCGGTGGCGACAGGCAACCGCGCG  
 CATCCGCGTGATGGTTCTGGATCGGAACGACCAACGACCCAGCGTTTGTCTCAGCCGAGTACCGCGCGAGCGTTCC  
 GGAGAATCTGGCCTTGGGACGCGAGCTGCTGTAGTCAACGCTACCGACCTGACGAGGAGTCAATGCGGAAGT  
 GAGGTATTTCTCCGGTATGTGACGACAGGCGCGCCCAAGTTTTCAAACTAGATTGTAATTACAGGCAATATC  
 AACAAATAGGGGAGTTGGACCAAGGAGTCAAGATTCTACAGATGGAAAGTGAAGCAATGGATAATGACAGGATA  
 TTCTGCGCAGGCCAAAGTCTTGATCACTGTTCTGAGCGTGAACGACAATGCCCCAGAAGTGGTCTCACTCTCT  
 CGCCAGCTCGGTTCCCGAAACTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAATGACCAAGATTCTGA  
 GGAAACCGGACAGGTGATCTGTTTATCCAAGGAAATCTGCCCTTTAAATAGAAAAATCTTACGGAAATTTACTA  
 TAGTTTATGTCACAGACATAGTCTTGGATAGGGAAACAGGTCTCTAGTCAACAACTCAAGTGAACCGCACTGACCG  
 GGGAAACCCGCGCTTATCCAGGAAACTCATATCTCGTGAACGTGGCAGACCAACGACCAACCCGCGGTCTT  
 CCTCGAGGCTCCTATTTCCGCTTATATCCAGAGAACAACTCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
 GACCCAGCTCGTCTCAAGGAGAACCCGAGATCACTTATCTCCCTGGCTGAGAACCACTTCAAGGGGCAAGCTATC  
 GTCTCCAGTGTTCATCAACTCCGACACTGGGGTACTGTATGGCGTGAAGTCTTCTGACTACAGAGCATTTCCGAGA  
 CTTGCAAGTGAAGAGTATGGCGGGGACCAACGGGCAACCCGCGCTCAGCAGCAACGTGTGCTGTGAGCTTCTGCT  
 GTTGACCAAGACGATAGCTCCGAGATCTGTATCCCGCGCTCCCAACGAGCGTTCCTACCTGGCTGGAGCT  
 GGCTCCCGCTCCCGCAGAGCCCGGCTACTCTGTGACCAAGGTGTGTGGGTTGACAGAGATCTCCGGCAGAACGC  
 CTGGCTGTCTACCGTCTGTCTAGGCGCAGCGAGCCGGACTTCTCTGGTGGTCTGACAGCGGGCAGGTGCG  
 CAGCGCGCGAGCCCTGTGACAGAGAGCGCGCTCAAGCAGAGCTCTGATGAGCCGTCAGAGCAGCGGCGAGCTCG  
 CCTCTCTCCGCCACTGTCACTGCTCACGTTGGCGCTGGCGGACAGCGATCCCCAAGTCTTGCGCGGACCTCGGCG  
 CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACTCACTCTGTACTGGTGGTGGCGGTGGCGCGGCTCTCTG  
 CGTCTTCTGGCTTCTGTCTCTGCTGCTGGCGCTCAGGCTCGCGCGCTGGCACAAGTCAAGCTCTGCTCGAGG  
 TTCAGGAGGCGGCTTGAACAGGAGCGCGGCTCGCACTTTGTGGGCGTGGACGGGTGACAGCTTCTCTGCAGAC  
 CTATTTCCACAGAGTTTCCCTCACCGGACTCGCGAAGAGTCACTGATCTTCCCGCAGCCCAACTATGACAGA  
 CATGCTGTGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTCTCAGGTGATTCGGTATTTTCTAAAGA  
 CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAAATCTTCTTTCTTTTCTTTTAAATGCTCTGTCTCCCAAGC  
 TGGAGTGCAGCGGTACGATCATGCTCACTGCGGCTCAAACCTTAGGCTCAAGCAATATCCCACTTTGGCT  
 CGGGTGAACAGGAGTCAAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT  
 CTATCTATCTATCTATCTATCTTTTGTGACAGCGGAGCTCAAGCTGTAATCCCACTACTTTGGGAGCG  
 CGAGGCGGGTGGATCACTCAGGTGGGAGTTTGAGACGACGCTGACCAACATGGGAGAACCCGCTCTATACTAA  
 AAAAAACAAATAGCCGGGCTGGTGTGATGTCTGTAATCCAGATCTGTGGAGGCTGAGTCAGGAGTGT  
 TGCTTTAACTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACCTCAAGCTGGGCAACAGAGTGT  
 AAACCTCATCTCA

0978191.101501

## **FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGLLLGTLWETGCTQIRYSVP EELEKGSRVGDISRD LGLPRELAER  
GVRIIPRGR TQLFALNPRSGSLVTAGRIDREELCMGA IKCQLNLDIIMEDKVKIYGV EVEVR  
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAF AQPEYR  
ASVPENLALGTQLLVVNATDPDEGVNAEVRY SFRYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN  
DQDSEENGQVICFIQGNLFFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVS LVSVTAHDPDCEENAQITYS LAENTI  
QGASLSSYSVINS DTGVL YALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSL FVLDQNDN  
APEILYPALPTD GSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTAVADSI PQVLADLGSLESPA  
NSETSDLTLYL VVAVAAVSCVFLAFVILL LALRLRRWHKSRLLQASGGGLTGAPASHFVGVD  
GVQAFIQTY SHEVSLTTDSRKSHLIFQP NYADMLVSVQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFLFFFNCSVSQAGVQRYDHSSLRPQT PRLKQLSHLCLRCNRD YRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGS LTFV I PVLWEAEAGGSPEVGS LRPA

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

## FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT  
ACAGCTGCCCCTGTAAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCAGAGCAAGAAATACCTGTGTTTCAGTCCATCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCCTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTTCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGTGCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCCTGGAGG  
CCCCCTGGTGTGTGATGTTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTTGAATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTT  
CTGGTTC

## **FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMLLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQQLLCGGVL  
VGGNWWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

# FIGURE 160

GGCGCCGGTGACACGGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCCTGCGCGCCCCGGCCCCG  
CGCGCCGCCACGCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCCG  
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGCCCGGCCCGCCCCGCCCCG  
CCCCGGCCGGCGGGGAACCGGGCGGATTCTCGCGGTCAAACCAACCTGATCCCATAAAAAC  
ATTATCTCTCCCGGGCGGCCCGGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCGCCCGCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGCGCGGCCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGCGGCCCGCCCCGAAACGACTTTTCAGTCCCCGACGCGC  
CCCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCGAGGCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCCAAGGTGACGACAAGCTGCCCGCAGCAGGGCCTGCGAGCTGTGCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTCTTGACGCGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCTTCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCTTGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCCTGCCACATTCCACGGCTTGGGCCGCTTACACAGCTGCACCTGGACCGC  
TGCGGCTGCGAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACACGCGCTGCAGGCACTGCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTTTCTGACGGCAACCGCATCTCCAGCGTGCCCGAGCGCCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCTACTGCAACGAGAACCAGCGTGGGCCATGTGCAACCGCATGCCCT  
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAACATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCGGGGACGCCCCACTCTGGGCCCTGGCTGCAGAAAGTTCCGCGGCTCTCTCTCCGA  
GGTGCCCTGCAGCCTCCGCAACGCTGGCTGGCCGTGACCTCAAACGCTAGCTGCCAATG  
ACCTGCAGGCTGCGCTGTGGCCACCGGCCCTTACCATCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGCGAGGCAATGCGCTGAAGGGACGCGTGCCCGCCCGGTG  
ACAGCCCGCCGGGCAACGGCTCTGGCCCCAGGCAATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCACTGCGGCCCGAGGGCTCCGAGCCACCGAGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGACGCCACT  
GCCGTCTGGGCCAGGCAGGACGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTACCCCCCTGGGCCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGCGGCCGACCCGTGGGGCAGGCAGGCCAG  
GTCCTCCCTGATGGACGCTGCCGCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGACGCGCTTGTTCAGAACCGCCCTCCCAACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTGTGTAATAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

## FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDP  
TFHGLGRLHTLHLDRCGLELGPGLFRGLAALQVLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHQNVRVAHVHPHAFRDLGRIMTLYL FANNLSALPTEALAP  
LRALQYLR LNDNPWVDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGC  
VATGPYHP IWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:**

**Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

# FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACCTGGGGACTTTTAC  
 AGTCCCACAGAACCGTCCCTCCAGGAAGCTGAATCCAGCAAGAACATGGAGGCCAGCGGGA  
 AGCTCAATTGCAGACAAAGCAAGTCTTTTTTCTCTTTCTCTTTTGGGCTTATCTCTGGCG  
 GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAAACTGAGGGCAGCTCCTTTGTACAC  
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATCTCCAGGCCGGGGTTAGGGTTG  
 TTTCCAGAGGGGAACAAACTACATTTGCAGCTCAATCAGGAGACCCGCGATTGTGTCTAAAT  
 GAGAAATTTGGACCGTGAGGATCTGTGCGGTACAACAGAGCCCTGTGTGCTACGTTTCCAAGT  
 GTTGTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG  
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
 TATAATCAGCCCCAACTCTATTTCGGGTCTCACCCGAAACGCAGTGTGGCAGGAAT  
 ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAAAC  
 CTCACAGCAGCTGGATGGTGGCTCTCCGCCAGATCTGGCAGCTGCTCAGGTCTACATCGAAGT  
 CTTGGATGTCAACAGATAAGTGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGAGATCTCTG  
 AGGACAGTCCGGTAGGCTTCTCTGGTTGTGAAGTCTCTGCCACGGATGTAGACACAGGAGTC  
 AACCGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT  
 CAATCCCTTGACCGAGAAATGAACATAAAAAACAACCTCGATTTCGAAAACCTTCAGTCTT  
 ATGAAGTCAATATTGAGGCAAGAGATGTCTGGAACCTTTTCTGGAATAATGCACCGTTCTGATT  
 CAAGTGATAGATGTGAACACCATGCCCCAGAAGTTACCATGTCTACGATTACCGCCCAAT  
 ACCTGAGAACCGCGCTGAAACTGTGGTTGCACCTTTTCAAGTGTTCAGATCTTGATTACAGGAG  
 AAAATGGGAAAATTAGTTGCTCCATTAGGAGGATCTACCTTTCCTCTGAAATCCGCGGAA  
 AACTTTTACACCTACTAACCGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAAATACAACAT  
 CACTATCACTGTCACTGACTTGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
 TGATCGCCGATGTCAATGACAACGCTCCCGCTTACCCAAACCTCTACACCTGTTCGTGTC  
 CGCGAGAAACACAGCCCCGCCCTGACATCCGACGCTCAGCGCTACAGACAGAGACTCAGG  
 CACCAACGCCAGGTCACCTACTCGCTGTGCGCGCCCGAGGACCCGACCTGCGCCCTCACAT  
 CCTGGTCTCCATCAACCGCGACAACGCCACCTGTTTCGCCCTCAGGTCTCTGGACTCAGAG  
 GCCTGACGGGGTTCCAGTTCCGCGTGGCGCTTCAGACCACGGCTCCCGCGCTGAGCAG  
 CGAGGCGCTGGTGCAGCGTGGTGGTGTGGAGCCCAACGACAACCTCGCCCTTCGTGCTGTACC  
 CGCTGCAGAACGGCTCCGCGCTCGGCCACCGAGCTGGTGCCTCCGGGCGCGCAGCGCGGGTAC  
 CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGACGCTGGCTGTCTGTACCA  
 GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCAATGGCAGGTGCGCA  
 CCGCCAGGCTGTGAGCGAGCGCGACCGCGCCAAAGCACAGGCTGGTGGTGTCTGGTCAAGGAC  
 AATGGCGAGCCTCCGCGCTCGGCCACCGCACGCTGCAAGTGTCTCTGGTGGACGGCTCTCTC  
 CCAGCGTACCTGCTCTCCGCGAGGCGGCCCGACCCAGGCCAGGCGCACTTGTCTACCG  
 TCTACCTGGTGGTGGCGTGGCTCGGTGCTTCTGCTCTTCTCTTTTCGGTGTCTCTGTTT  
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCTCGGTGGTGTGCTGTTGGTGGCCGA  
 GGGCCCCCTTCAGGGCATCTTGTGGACATGAGCGGACACGAGACCTATCCAGAGCTTACC  
 AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGACCAATGAGTTCAAGTTCCTGAGCCGATT  
 ATCCCAACTTCCCTCCCGAGTGCCTGGGAAAGAAATACAAGGAAATTCACCTTCCCCAA  
 TAACTTTGGGTTCAATATTCACTGACCATAGTTGACTTTTACATTCATAGGTATTTTATTT  
 TGTGGCAATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
 TTACTCTGATTTTTCTCATGTTCTTCTCCCTTGTGTTTTAAAGTGAACATTTACCTTTATT  
 CCTGGTCTT

## FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKILICRQRQVLFSFLLGLSLAGAAEPRSYSVVEETEGSSFFVTNLAKDLGLEQREFSR  
RGVRVVS RGNKLHLQLNQETADLLLNEKLDREDLCGHTPCVLR FQVLLES PF EFFQ AELQV  
IDINDHSPVFLDKQMLVKVSESSPGTTFPLKNAEDLDVGQNNIENYIISPNSYFVLTRKR  
SDGRKYPELVLDKALDREEEAE LRLTLTALDGGSPPRS GTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFVLVVKVSATDVTG VNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPLFLKSAENFYTL LTERPLDRESRAEYNITITVTDLGTPMLITQ  
LNM TVLIADVNDNAFAFTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTSYLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSS EALVRVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELG LFGVWAH  
NGEVRTARLLSERDAAKHRLVLVLVDKNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTAQ  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGP LPHGLVDMSGTRT  
LSQSYQYEVCLAGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

### Important features:

#### Signal peptide:

amino acids 1-26

#### Transmembrane domain:

amino acids 685-712

#### Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

#### N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

0907091-10501

ACCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCGCGTAGCCGTG  
 GCCGATTGCCTCTCGGCTGGGCAATGGTCCCGGTGCCGGTCGACGACCGCCCCGCGTCAT  
 GCGGCTCCTCGGTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCGCTCCGCGGCGTGG  
 AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
 GGGGCTGTGTACCTGGGTGAGGAGGAGCTCTGCATGCCCGATGGGCCAGGACAGGGGACG  
 AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
 TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTACAGAGCCTAGCGGCGTCACCTGTGGTGCT  
 GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTGGATGGCGCTGG  
 AGCACACTTCCCTGCACAGAGAAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
 CAGCCCCGACAGGAGACTCCAATAACACTGAAAGTCTGAAATCCCCAAGGTGAACCTGTGAG  
 GAGAGAAACATTACAGGATTAGAAAATTTCACTGTGAAATTTAAATATGTACACGAGACT  
 TATGGATTTTCTGAACCAAAACGGTAGTGACTGTACTAGTCTGTTTATCACCCCGTGGT  
 GCCGCTTTTCTGCCAGTTTGCCCCCTCACTTTAACTCTCTGCCCGGGCATTTCCAGCTCTT  
 CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTTACCAGGTTTGGCACCGTAGC  
 TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC  
 GAACACTGGAACACTGAAAACTTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAA  
 GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTTCCCAGCACTTTGATAAAAAGTGTGGA  
 CTGGTTGCTGTATTTTCCCTATTCTTTTAAATAGTTTATTATGTATGCTACCATTCGAA  
 CTGAGAGTATTCGGTGCGTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
 GAAAGAAGTTGGAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
 CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
 CAACCTGAATGCTATAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
 AAAAAATTTCAATAG

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEEL  
ELLHDPMGQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEKVSSEPSGVTCGAGGAEDSRC  
NVRESLFLSDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETLETKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSDWLLVFSFLISFIMYATIRTESIRWLIPGQEQEHVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCTCGCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCTC  
TTTGCCAGCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTCTTCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGCCCCGACATGCTTGAGTGCAGCCGTTTCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCCTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCTATGGGACAGAAACAGGTTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAGAAATATTCAAAC TAATA  
AAATCATGAATATTTTAA

## **FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLD ETIQCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGGLVITSVKRWQKQREFKRISRSIRKLQC

**Important features:**

**Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

## FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGTGCCTTGTGGTTCACAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCTTGTGGCCAATGTGCT  
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGCGTCGTCTGCCTGTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCAACCCG  
CCCTCTGCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTATCTCGGTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTGTG  
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCGGTGGCCATGGAGTTGGCGGTGCA  
GTGTTCTTCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGCTCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCG  
CCTGTGCACCTTCTTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA  
GTGCACGGCAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCGTGGCGAAGGCCAGCAGCCACCGACGCGCCCTCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA  
TGGAGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

## **FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988  
><subunit 1 of 1, 560 aa, 1 stop  
><MW: 58427, pI: 6.86, NX(S/T): 2  
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN  
PFAFLMGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSFVLV  
KKGEDIPLMLGVYITIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFALLEQILCASGHSSGFGSLCGALFITFGILGALGPPYVDRTK  
HFTEATKIGLCLFSLACVFFALVSQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLAMTALTVRREPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

# FIGURE 170

GTCCACATCTGCTCAACTGGGTGAGTCCCTCTTAGACAGCTCTTGTCATCATTTGCTGAAAGTGACCAAC  
TAGTTTCCCAAGTAAAGGGGTCTCCCTTGGCAATTTCTTGATCGGGCTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGCCCTTCCTCTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGTGTGTCGGGCGAGCTCTGGGGG  
AAGGAGACCGGGCTGTATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCTTTGAAAGAACTCTAGTGGTT  
TCTGAATCTAGCCCACTTGGGGCTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTTGTCCAGAGGTGACCACTCTCCAGGTGAAATACCAAGTGTCCAGGGAAGTGCC  
ATCTGTGTACAGTGTACGGAGACTGTCTCCAGGAACTGGGCGGGAGGAGGCGGAGGCTCAGGCTGGGGCGCCCTCT  
CCAGCTGTTGCACTGCTCCTCAGGCGCTCCCCATTCCAGGTGGAATCTGAGTGTGATTTCTGTATGTGCTTGGCACAAGGGGATTT  
GCTCTGTAGTGTGTGAGATCTCAAGTGTCTGGACATCAATGACCAACAGGCAAGCTTTCCCAAGGGCGAGCAGGA  
GCTGGAATCTCTGAGAGCGCTCTCTCTGCGAACCCGGATCCCTCGGACAGAGCTCTTGACCCAGACACAGGCCCC  
TAACCACTGACACCTTACATCTGTCTGCCAGTGAGCACTTTGCTTGGATGTCAATTTGGGCGCTGTATGAGAC  
CAAACTGACAGAACTCATAGTGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTGTATCTGGTGTAACTGCT  
CTATGCAATGGGAAACCCCGGAGTCAGGTACCACTTGGTCAAGGTCAAGCTCTGGATCCCAATGACAATAG  
CCCTGCGTTTGTCTGAGAGTTCACTGGCAGTGGAAATCCAAAGAAGATGTGCACTGTGACGCTTCTCATAAAT  
GACCCGACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTCTCAGTAAGCACATGCTCCAGAGGT  
CTGGACACCTTCAGTATTGATGCAAGACAGGCCAGGTCACTTGCCTCGACCTCTAGACTATGAAAGAAACCC  
TGCTTACAGGTGGATGTTCCAGGCAAGGACCTGGGTCCCAATCCTATCCCGACCTATTGCAAGGTTCTCATAA  
GGTTCTGGATGTCAATGACAACTCCAGCATCCAGCTCATATGGGCTCCAGGCTCATCTGGTGTCCAGAGG  
TCTTCCCAAGGACAGTTTATTTGCTCTTGTCTGATGGCAGATGACTGGATTTCAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCCAAGAGCTGGGGCACTCCAGGCTGAAAGAACTAAATGGGACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGGCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAGAAAGACAGCTCAGCATTCAGATCAGTGCATCAACGACAATGCACCTGTGTTGAGAAAGCAGGATGATG  
AGTCTCCAGCGGGAAACAACTTACCTCTCTTCACTTACATTCATCAGGCTCATGACGAGCTCTGGGCACT  
TAATGGAAGAAGTCTCATACCGCATCCAGGACTCCCGAGTTGCTCACTTAGTAGTATGATCTCAACACAGGAGA  
GGTCACTGCTCAGAGTCTCACTGAATATGAGAGATGGCCGGCTTTGAGTCTCAGGTGATCCGAGAGGACAGCGG  
GCAACCTGCTCTGCACTCAGTGTCTCTGTGTGGTTCAGCTCTTGGATGGCAATGATATGCCCCAGGAGTGGT  
CCAGCTCTGTGCTGATGATGGAAGGACCGCTCTCTCGTGTCTTGAATGCTGCAATGCATGCTCCAGCTGCTGGT  
CTCTGAGACTCCCAATGGCTTGGGCCACCGGGCACTGACACACCTCACTGGCCACTCAGCTCCCGGCCATT  
CTTTTGGACAACTATTGTGGCAGAGATGACAGTCTGGGGCAATGAGAGGCCCTCTACAGCTCCCGCAATGG  
AAATGAAGCCCACTCTTCTATCTCAACCTCTCATACGGGGCAGCTGTTGCTCAATGTACACAAGTCCAGCAGCT  
CATTTGGAGTGAAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGGAAGCCCGCTTCCAGACCGAGCCCTGT  
GAGGCTCATGTTTGTCTCCAGTGTGGACCACTGAGGAGCTCAGCCCGCAAGCTGGGGCTTGAAGCATGTGAT  
GTGTCAGGTGATTTGCTCGCTGGTGTACTGTTGGGCATCTTCGGGTGATCTTCGCTTGTGTCATCTGCGG  
GACAGAAAGAAAGAGACACAGGCGCTCAACTGTCCGGAGGCGGAGTCCACTTCCGCGCAGCAGCCCAAGAGGCC  
CCAGAAACACATTTCCAGAGCGACATCCACTCGTGTCTGCTCAGGGGTCCAGGCGAGTGAAGCTTTGAAAT  
CGGCGACTCCCAAGATGTGGACAGGAGGCGATGATGGAAGCAGGCTGGGCCCCCTGCTCGAGGCGAGCCGAGG  
CCACTTCAACCCAGCTGTACAGGACGCTGCGTAAATCAAGGCAACAGGAGGACCCGCGGAGAGCCGAGAGGT  
GCTGCAAGACAGCTCAACTCTCTTTCAACCATCCAGGCGAGGAAATGCTCCCGGAGGAACTGAACCTTTCC  
CGAGCCCGAGCTGTCACAGGCGCACAGCTCTCCAGGCTCTGAAGGTTGAGGAGCGCCCAAGGAGAGCTGGC  
TGGAGACAGGCGCTGAGGAAGCCCAACAGAGGCCCAAGGCTCCCTCTGCAACCTCGAGACGCGACGACATCT  
CAATGCGAAGATGTCTCCCTGGAAGAAAGATCAGGCGCCCGTGCAGATCTCTCGGAGCTGGTCCGCTGTCTGTGG  
TGCTCTCCGAGCGGAAGCCCGTGGAGGAGCTCACTGTGGATTTCTCTGTTGTAGCAATCTCCAGCTGTCT  
GTCTTGTGTCATCAGGCGCAATTCAGGCCAAACCAACCAACGAGGAAATAGTACTTGGCCAGGCCAGGAG  
CAGCAGAGGTGCAATCCAGGACAGATGCGCCAAAGTGCAGGCTGAGGCGCAGGACAGCCAGAACAGGAGGA  
AGGCGCTTTGGATCTGAAGAGGACCTCTCTGTGAAGCACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCT  
CAGCAGAGTGTGCGCTCGGACGAGCTGAGCGCCCTGACCCGCGCTGGATGGCGAGACTCTCTTGGCCCTCAC  
CAACCACTACCGTGAACAATGTGATCTCCCGGATGCTGAGCGACGAGGAGGACGAGGACCTTCCAGAGCTTTCG  
CAGGCGAGAGGCAACAGAGCTGAGCCCAACAGGCGCAGGCTGGCAGCACTTTGTCTCGGAGATGAGCTACT  
GCTGGAGATGCTGCTGAACAGCGCTCCAGCATGCCCCGTGGAGGCGGCTCCGAGGCGCTGCGGCGCTCTCGGT  
TCTGGGAGGACCTCATGTTTGAATCTTGGCCAACGATGCGACTCAGGCATGAAAGTGAAGGGGACCCAGGTGG  
AAGAGCGGGGACTGAGGCGCAAGGACAGGAGCAGGCGCAGCAGCAGGAGTGGCTGGAACATACCTCAACGCTCT  
CTGGATCAAGAAACAGGGGCTGAGGATCTGTGGACAGAGCTGTTTCTTAAATCTGTGAACCTCACTAGCTAG  
CGGCGGCTGAGAACTTTAGGTGATGTATGCTACCCCAACAGAGGAGGCAAGAGCCCGAGGACTCAAGCTGAC  
TGACCAAGAGCGCCCTTTGAAGCACTCTGAGTCTTTGGAGGACAGGAGCGTTTGTGGCTGAGATGAATGTTT  
TCTTGGCAAAACATATGTGGACCAAGGGTCAGTCTCTTGGCAGAACAGATGCCAGGAGTATCAGGCGAGG  
AAGAGGTGGCTCTTGGGTGACGAGGTGACCTTGGGGGTGTCAGGAAATGCTCTCTGACCTAT  
CAATAAGGAAAGCAGTAAAAAAGGAAAAAAAAAAAAA

0373137.101501

## **FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLQLQLLLGLLGPGGYLFLLGDCQEVTTTLTKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPLCVSFVDVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLTSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLSDNNSPAPAESS  
LALEIQEDAAPGTLTIKLATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDVNDNIPS IHVTWASQPSLVSEALPKDSF  
IALVMADDLDLSDGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLQAQD  
QGLQPLSAKKQLSLQISDINDNAPVFEKSRYEVS TRENNLPSLHLITIKAHADALGINGKVS  
YRIQDSPVAHLVAIDSNTEGVTQAQSLNYEEMAGFEFQVIAEDSGQPM LASSVS VVWSLLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDPPLATHSSRPFLTT  
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMMLTVICLAVLLGIFGLILALFMSICRTEK  
KONRAYNCREAESTYRQPKRPQKHQKADIHLVPVLRGQAGEPCEVGQSHKVDVKEAMMEA  
GWDPCQLQAPFHLTP TLYRTLNRQNGQAPAESREVLQDTVNLLFNHPQRQNASREN LNLPEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAAFAERNPVEELTVDSFPVQISQLLSLLHQGFQPKPNHRGNKYLAKP GGS  
RSAIPD TDGPSARAGQTDPQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTNTYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEM LLEQRSSMPVEAASEALRRLSVCGR TLSLDLATS AASGMKVQGD PGGKTGT EGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTGAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAATTTCTTGCACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAATGAACCTGTGTGTAATTCTGTGTGATCCTGGTTTTTCATGGTGCCTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGAAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTCTGAGTTTGGTGTGTCAACTGCCATACACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTTCTGGGAATGATAAAAAGTGTACCACCTTCAGCATCAGG  
AAGTGAAATCTTACTCTTATTCACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAACAGCTGATCTATATGTCTACCAAGGAGAGAATAGAATACTCCAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAAATTT  
CATGGCTACCATCAATATGTTTTGATCGAGTTGGGAAAACGGATCCTGTCCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT  
TCCTTCATTCTGTGTTGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTATTGTCTGTCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTTTAGAA  
TACCGCACCATAACTACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACCTTAAGCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCGAGGCTGACATTTTATAAAC  
AAACAAATGCTATGGTAGCATTTTTACCTTCATAGCATATCCTTCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTCACATGAAAAGGTTATAGCTTTGCTTGAAGTTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGGCGGCGGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTATTGACAGCTTATAATG

## **FIGURE 173**

MSFLIDSSIMITSQILFFFGWLFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTIFYFF  
WKLGDPPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTIIQ  
QEVDALEELSRLFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## **FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAAATTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTINTNTNGGAAAN  
TAGGAGATCCCTTTCCCATTCCTC

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

## **FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDWPWASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCG  
RPQGHQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRILPVPANSYFGFSDSGKGLVRAEELSFFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPDILIVGAPYFFERQEELGGAVVYVLNQGGHWAGI  
SPRLRCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDKVFIYHGSSLGVAKPSQVLE  
GEAVGIKSFYSLSGSLDMGNGQYPDLLVGLSADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRCVFSYIAVPSSYSPTVALDYVLDADTDRLRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQPSQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGGQPVIGLELMVTNLPSDPAQPOADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAVQVTFYILSTSGISIEETTELEVELLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGGSLRTLGSFAFLNIM  
WPHEIANGKWLlyPMQVELEGQGGPGQKGLCSPRPNIHLHDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLPYSFDRAAVLHVWGRLWNSTFLEEY  
SAVKSLEIVIRANTIVKSSIKNLMRLDASTVIVPMVYLDPMVAVVEGVPWWVILLAVLAGLL  
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPPREGP  
DAHPIAADGHPGLPGDHPGPGTA

### **Important features:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 1040-1062

#### **N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### **Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

# FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAAACAAGATGCTCAAGTGTCAGCCGTA CTGTGTGTGTGTGCAGCCGCTTGGTGCACTCA  
GTCTCTCGCAGCTGCCGCGCGGTGGCTGCAGCCGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAACAAATGGCTACCCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCA CCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATAATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAAATGTGAAGGACATTGC  
CCATGTCTTTCAGATAAGCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTC AAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAACATTGCTGAGGCCCTGAGAGAAGCAGATTTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCTGTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTGGACAGTGTGGTGTGTTGACAGATATGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGAGATTT  
TGCTAGTGGCGATTTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAAATCTACATTTCTAATATTTA  
CAAAATGATAGCCTATTTAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGATAATTATTTGAAAAATTCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTCCTTTGAGTTTTATATTCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAGTCTACTATAATAAATTTTTCACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG  
ATAATCTAAGTGAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCACTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAA

## **FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRPERSRFDTSILPI  
CKDSLGMWFRNLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGYKPTQCHGSGVQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

# FIGURE 180

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAAACAGTACCTGACGC  
 CTCCTTCAGCCCGGATCGCCCCAGCAGGATGCGCGACAAAGATCTGCTGCCCTTCCCGTGTCTCTCTGCGCC  
 CTCTGCCCTCGGTGCTGCTGCTGCGGCGCGCCGCTTCCACCTTCCCTCGATAGCGACTTCACCTTTACCTCTT  
 CCGCCCGGCGCAGAAAGGAGTCTCTTACCCAGCCATGCCCTGGAAGGCTCGCTGGAGATCGAGTACCAAGTTTAA  
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA  
 TCAGATGGAGTTCCACCTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTCAGCACCAAT  
 TCTGAGAAGGTGATTTTTCTTGAATTAATCCTGGATAATATGGGAGAACAGGCAACAGAACAGAGATTGGGAA  
 AATATATATCTGCGCACAGATATTTGGATATGAAACTGGAAGACATCTCGGAATCCATCAACGACATCAAGTCC  
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCATTGAAGCTCTGATCGAAACATACAGAAAGAC  
 AACITTTGATAGAGTCAATTTCTGGCTATGGTTAATTTTAGTGCTCATGGTGGTGTGACGCCATTCAGGTTTTAT  
 ATGCTGAAGAGTCTGTTTTGAAGATAAGAGGAAAGTAGAATCTAAACCTCCAAACTAGAGTACGTAACATTTGAAA  
 AATGAGGCATAAAAATGCAATAAAGTGTACAGTCAAGACCATTAATGGTCTCTCCAAAATATTTTGGAGATATA  
 AAAGTAGGAAAACAGGTATATTTTAAATGTAAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
 TTGTACTTAAGTGTGTAAACAGGAATATTTTGCAGAAATATAGGTTTAACTGAATGAAGCCATATTAATACTGCAT  
 TTTCTTAACCTTTGAAAAATTTTGCAAATGTCTTAGGTGATTAAATAAATAGATATTGGGCCATTAATGCAACACC  
 AGTCTGTTTTTAACAGGTTCTATTTCCAGCAACTTTTTTGAATGCGGCGAGTTACAAATTAACCTGTGGGAAGTTT  
 TCAGTTTAAAGTTATAAATCACTCGAGAATTAACCTAATGATGGATTGAATAAATCTTTAGACTACAAAGCCCAAC  
 CTTTTCTCTATTACATATGATCTCTCTATAATGTAATAGATAATAATAGACTTTGAAATCAATTAAGTGTTTTTG  
 AGATTTTTTATAACCAATACATTTCACTGTGAACATATAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC  
 CAAAAGCTGACATTTTCAGATTCTTAAAAACAACAAAGTTTACATTTACTAAAAATTAGGCATGTTTTCTCTTTG  
 AAATGAGAATATAGTTTTAAAGCTTCTCTCCCAATGGGACACATTTTCTCTAACCTTTACTAAGTGTAGGA  
 TTTTAAAAATTAAGTGTGAGGTAAAAAAGTTTTATTTTTAAATAGTATCTGTCAAGTTATAATCTGTGCAAGTTAA  
 TAATCATGTATGTATTTTAACTATGATTGCTGACTTGGATAATTTCAATTTACACAGAGTTATGAGGAAAAATA  
 TTGCTAAATGATCTGGGCCATCCATAAATAAATATCTCCCTTTCTGAGCTTCAAGAAATATCAGAAAAACAGGAA  
 AGAATTTAGAAAAACTTGAGAAAACTTAATCCAAATAAATTCACCTTAAGTAGAACATATAAATAATCTAGAA  
 ATCTGACTGGCTCATCATGACATCCCTACTCATAAACATAAATCAAGGAGATGATTAAATTTCCAGTTAGCTGGGAG  
 AAATCTTGCTGTAGGTTTTTATTTTTCTACAAGAAATCTGTTTGAATTTATTTTAAAGCAGGTACATTTTTATA  
 AAATGTAAAGCCCTACTGAAGTTTAGCACTGGGTGTACATATTTATAAAAATTTTTATATATAACAACTTTTTAA  
 TAAAAAGTGAATTAACCATATATACAAAGAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTTAC  
 TCAAGTACTAGTAATTTAACTCATCATGAATGAACATTAATTTTTAAGTTATGCCCATTTATAACGTTGTTTTAT  
 GACTACATTTGATGTTAGAAACAACTTAAATTTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATTT  
 CTTGATGAGCAATTAATGAACAGGAGAGTATTTCAATTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCT  
 TCTTAGGCCCTGGGAGAGAGCAGCTTAGATTTCCTACTGGCAAGGTTTTTAAAAAATGAGGTAAATGCCGATAT  
 ATGATCAATTTACCTTAATTTGGCCAAAGAAAATGCTTCAGGTGCTAGGGGTATCCCTGCAACACTTCGAGAACAA  
 AGGTCAATAAGATCCTTGCTATGAATACCCCTCCCTTTTGGCGCTGTAAATTTGCAATGAGAAGCAAAATTTACA  
 GTACCATAACTAATAAGCAGGGTACAGATATAAAGTCTGATCTTTCTATAAAAGTGTGATTAAGAACTCTA  
 CCTCTCTGTATGGCTGTACTGTACTGTACTCTCTGACTCCTTACTCTAACCAATGAATTTGTTACATAATCTTCT  
 ACATGATGATTGTTGCGCACAGATCTTAAACCTATGATTCAGTAACCTTACCATAAAGAACAGATAATGCTCT  
 TATTTGGAAAAAGAAATTTAGGAATACTAAGGCAATTTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
 CATAACCAAAAAAGCAAACTTTGTAACAGAGTAAAAATCTTTAAATTTCTAAAGACATAGCTGTTTATCTGCTCT  
 CATATGCTTTTTTAAATTTTCACTATTCATTTCTAAATTAAGTTATGCTAAATTTAGTAAGCTGTTTATCACTTT  
 AACAGCTCAATTTGTCTTTTTCAATACAAATTTTAAAAATACTACAATATTTATGGTAAAAATTAATGCTCTTTA  
 CATAAATGTAGCAGTACCGGTGTCACTCACACTAAGGCCCTAGAGTTTGTCTGATATGCAATTTGATGATTAAT  
 GTTATGCTGTTCTTTTCACTGTAAGTCAAGACATGAGGGGTGTTGTAATTTTATGGTAAAAATTAATGCTCTTTA  
 CACATAATGGTGTCTTAAATTTGACAAAAAATGAGCATTACAAATTTGATGCTCTCTCAATGAAGATCTTTTAT  
 GTAAATTTTAAAAAGCATTTGATTCGCGATGTAAGGATTTTTCATCTGAAGTAAAGTATGCAAAATCAGTGTG  
 CTCAAATGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGATATATAATAA  
 AAATTTACAAAGAAAA

## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFLLPAGQKECFYQPMPLKASLEIEY  
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFTSTISEKVIFFEL  
ILDNMGEQAQEDEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

REF ID: A67340

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACAGATG  
CTCACCAGAGAGTTCGAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTGGATG  
CTGCTTTCTGCTCATTCTCCTGTGTCAAGTTCAGAGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTCAACAAATCTTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTCGGTGAGGAGCATTAG  
TAACAGCTACTCATACTCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCTTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCTTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCTTGGGAAGAATAATTTCTCCCAAACTGCCTCACTGACTACCTTGTCTGATGATCTCTC  
TCTTTTTCTCTTTTCTTCTACCTTCACTTACGGCTTTTCTCTGCTCTTCCATGTCTTGAGATC  
TCAGAGAATAAATAAAAAATGTTACTTTATAAAAAA  
AAAAAAAAAAAAAAAAAAAA

[illegible]

&lt;MW: 19330, pI: 7.25, NX(S/T): 1

amino acids 146-171

[illegible]

CCAGTCTGTGCCACCFCACTTGGTGCTGCTGTCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCGGGACCATGCGGGGGGACGCGGCTGGCGCTCTTGGCGCTGTTGCTGGC  
TGCCTGCGGAGAGCTGGCGCGGCCCTGCGCTGTACTGCTTGTCCGGAGCCACAGGAGTGT  
CGGACTGTGTACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCTGCCGTGCTCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTTGAGATCCCCGCCCAACCCCATGGCCCTATGCGGCCCA  
GCCCGGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

## **FIGURE 185**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGCATGG  
TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCACTCAGCGCCGCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCGCGGAGGGGACGCAAGGCTGCAAACTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGCTT  
CTGATCAAAATCATTTCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGTCTGTCT  
TTGCCGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGACA  
GACACTAAACCCAGCTATCCAATGCACTGAACTCCTTTTATATAATAGATGCTATGAAAAC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG  
TGATTGCAGTAAATTACTGTATGTAAATTCTCAGTGCGCACTTACCTGTAAATGCAATGA  
AACTTTTAAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

00072151 101541

&lt;subunit 1 of 1, 266 aa, 1 stop

MMALGAAGATRVFVAIVAAALGGHPLLGVSATLNSVLNSNAIKNLPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTDINDYQPPYCAEDDEECGTDEYCA\$PTRGGDAGVQICLACRKRKRKMRH  
AMCCPGNYCKNGICVSSDQNHFRGEBIEETITESFGNDHSTLDGYSRRTTLLSSKMVHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHKRKGSHGLEIFQRCYCGEGL\$CRIQ  
KDHHOANSS\$RLTTCORH

Signal peptide:

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

## **FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

## FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCTGCTGGTAGTCGCGCGGTGGCTGCACCTCACCAATCCCGTGCGCGCGG  
 CTGGGCGCTCGGAGAGTGCCTGTCTCTCTCCTGCACCGCGTGGCTGGGCTCGGCGGAGCGGGGCTCCGCCGCA  
 GGGTTTGAGATGGGSGAGTGTCTACAGGAAGCGACCCGCGATGGCAAGTATATTTTGTGGAAATGAAAGGA  
 AGTATTAGAAATAGAGCTGAAGACCATTCACAGATTAAATATTTTGGGGACAGATTTGTGATGCTTGATTCCACCT  
 TGAAGTAAGTAGACAGAAATCTCAAAATTCATATTAATCACTCAACTGGAAACAGCAGTGAATCTTAATGTCTCAC  
 TTAATCAAGAACTTGCATAGAAGAGGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGATCTGAAAG  
 GATCATCTCTGTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACATGTTTACTTGG  
 AGTGTCCAAAACCTGCAAGCAGTAGAGAAATTAAGACAAGCTTTCAAGAAATTTGGCAITTGAAGTTACATCTCGTATA  
 AAACCCGAATAACCCAAATGCAATGCGCATTTTTTAAATAATAATAGAGCATATGAAGTACTCAAAAGTGAAGA  
 TCTACGGAAGAAATGATGACAAATATGGAGAAAGGAGCTTGAGGATAATCAAGGTGCCGATATGAAGAGCTGGAA  
 CTATTATCGTTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAAATTGGAAAGAGAGAAATTTGATGC  
 TGCTGTTAATCTGGAGAAGCTGTGGTTTGAATTTTACTCCCGAGGCTGTTCACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTTACTTCAATTTGGAGCTGTTAACTGTGGTGTATGATGAAT  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAATA  
 TCATGGAGACAGATCAAGGAGAGTTTATGAGTTTTGCATGACAGATGTTAGAAATGACAGTGACAGAACTTTG  
 GACAGGAAATTTTGTCACTCCATCAACAACTGCTTTTGTGCTGGTATTTGGCTGGCTGATCACTTTTGTGTCAA  
 AGGAGGAGATTTTGTGACTTCACAGACAGGACTCAGGCTAGTGGCATGTTGTCTCACTCATTTGGATGTGATA  
 AGAAATATATTTGGAAGTATACATAATCTCCAGATTTTGAACACTTTTCGGCAAAACACATGACAGAGATCGTTT  
 GGCTCATCATCGGTGGCTGTTATTTTCAATTTTGGAAAAAATGAAATGACATCTGAGCTGAAAAAATCT  
 AAAAATCTACTTAAAAATGATCATATTCAGTTGGCAGGTTTGGACTTCCCTGCGACCGAGACTCTGTAGTAA  
 TCTGTATGTTTTCAGCCGCTCTAGCATGATTTAAAGGACAAGGAACCAAGTAATGAAATTCATCATGATGATA  
 GAAGATCTTATATGATCTTGCCTTTGCGAAAGAAAGTGAATTTCAATGTACCAAGCTTGGACCTGCAAAA  
 TTTTCTGCGCAATGACAAAGAACCATGGCTTGTGATTTCTTTCGCCCTGGTGTCCACATGTGCGAGCTTTACT  
 ACCAGAGTTTCAAGAGACATCAAAATCTTCTTTATGGTCAGCTTAAAGTTTGGTACATGAGATTGACAGATTCA  
 GGAAGTCTTAACTATGTATAACATTCAGGCTTATCCAAACAGTGGTATTAACCAAGTCCAACTGATGATGATA  
 TGAAGGACATCACTCTGCTGAACAAATCTTGAAGTTCTAGAGGATCTTATGATCTTCAAGTGTCTCCCTTAC  
 ACCCAACCCCTTCAACGAATAGTTTACACAAAGAAACACACGAAGTCTGGATGTTGTCTTATTTCTCCGCT  
 GTGTCACTCTGCCAGCTTAAATGCCAGAAATGGAAGATGGCCCGACATGATCACTGGATGATCAACGCTGGG  
 CAGTATGAATGGCCAACTGATCATCTTTTGTGCGCAGGAAACGTTCAAAGATACCCCTGAGATAAGATTTTT  
 TCCGCCAAATCAATAAAGCTTTTACGATCACAGTTTCAATGGTGGAAATGAGATGCTTATTTCCCTGAGAAT  
 CTGGGGTCTAGGATTTTTCAAGTATCCACAGATCAACACCTCAGACTTTCAGTGAAGAAAGTTCTCAAGG  
 GAAAAATCATTTGGGTGATTTGATTTCTATGCTCCTTGGTGGAGCTTGCAGAAATTTGCTCCAGAAATTTGAGCT  
 CTTCGCTAGGATGATTTAAAGGAAAGTAGGAAGCTGGAAGATGAGCTGTCAGGCTTATGCTCAGACATGCCAGAA  
 AGCTGGGATCAGGGCCTATCCAACTGTTAAGTTTTATTCTACGAAAGAGCAAGAGAAATTTTCAGAAAGAGCA  
 GATAAATACAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATGGAAATCTCCGAAATCAAGGCAA  
 GAGGAATAAGGATGAACCTTTGATATGTTGAAGATGAAGAAAGTTTAAAGAAATTTGACAGATGACATCAG  
 AAGACACTATTTAGAAATGTACATTTTATGATGGGAATGAATGAACATATCTTAGACTTGCAGTTGTATGCCA  
 GAATTTATCTACAGCACTGGTGAAGAAAGAGGCTGCAAACTTTTCTGTAAAGGGCGGGTTTATAAATATTTTA  
 GACTTTGCGAGCTATAATATATGTTTACACATGAGAACAGAAATAGAGTCAATCATGATTTCTTTGTTATTTGCT  
 TTTAAACAGACTTTTAAAAATATATAAACGATCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAGTCCATG  
 GACCATCAAGTTCGTTCCCGCTCAGCGGACTTATATGTTTCAGTGGCTGGCTTGAACATGAGTCTGCTGTGGCT  
 ATCTACATAAATGCTCAAGTTGTATAAAGTCACTTTCCCTTCAAGCTTTTTCGGTGCCTGAAAGAGGTAACCT  
 TAGTTTTTGGTCACTTGTCTCCCTAAAAAATGCTATCCCTAACCATATATTAATTCGTTTTAAAAAACACCAT  
 GATGTGGCAAGTAAACAAACCTGTTATGCTGTATATTATGAGGAGATTCTTCATGTTTCTTCTCTCTCA  
 AAGTTTGAAGAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCATATGTGCAACAGTAAAGTACAC  
 AAAATTTGAGCAACAGTAAGTGACAAATCTCTAGTTTGTCTGTATCATCCAGGAAACCTGAGGGAAGAAATTA  
 TAGCAATTAACCTGGGCAATGTGAGATGCTCTAAATGTTATCAAGTATTTAGTATTTTAAAGATATA  
 TGTGTTTCATGATTTTCTGAAATGCTTTTCATAGAAATTTTCCACTGATAGTTGATTTTGGAGCATCTAATAT  
 TTACATATTTGGCTTTGAACTTTGTTTGTGACCTGTATCTTTTATACATTTGGGTTTCTTCTTCATGTTTGG  
 TTTTTCACCTCTGTCAGTCTATTATTTATTTCAATAGGAAATTTACTTTACAGGTTGTTTACTGTAGCTTAT  
 AATGATCTGTAGTTTATTCAGTATCTAGTTTATCTGTAGAGGGCTGCCTTTTCAGATAAATATGACATAATA  
 ACTGAAGTTATTTTATAGAAATCAAGTATATAATCTAGGAAAGGATCTTCTAGTTTCTGTGTTGTTTGA  
 CTCAAGAAATCAAAATTTTCTGAGTAAATGATGTTTATGTTATAATTCAGATGTTACAGATGTTGAATTAAT  
 CCAATCAGTCAAAAGAGGCTCAATGAATTAAGAGCTTGCACTTTTCAAAAAAAGAAAAA

## **FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGT DQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNNPNAHGDFL KINRAYEVLKDEDLRKKYDKYGEKLEDNQGQYESWNYYRYDFGI  
YDDDPEIITLERREFDAAVNSGELW FVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRLCRMKG VNSYP SLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRS TVTELWTGNFVNS  
IQTAFAAGIGWLITFC SKGGDCLTSQTRLR LSGMLFLNSLDAKEIYLEVIHNL P D F E L L S A N  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYV F Q P  
SLAVFKGQGTKEYEIH HGKKILYDILAFAKESVNSHVTTLGLFQNF PANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEGHH S  
AEQILEFIEDLMNPSVVS LPTTTFNELVTQRKHNEVVMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFFPKSNKAYQYHSYNGWNRDAYS LRIWGLG  
FLPQVSTDLTPQT P FSEKVLQGNHWVIDFYAPWCGPCQNFAP EFELLARMIKGKVKAGKVD C  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEBQINTRDAKIAALISEKLETLRNQGRNKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

007691-101503

AGACAGTACCTCCTCCTAGGACTACACAAGGACTGAACCAGGAAGGAAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA  
GTCGTTGGTGAAGTTTTTTCATTCTCAGAGGAGAAAACTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGTGAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAGTGGGTGATGTAACAATCGTGGTGAATATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCGCGCTGTTGGCTTTTCACAGAGGTCTGACATCAGAACTTCAGGCCCT  
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTTGTGAATACTGGGTTACCA  
AAAATCCAAGCAAGATTATGGCCGTGATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GTGAAGTACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATCAATATCTTCTTGAG  
ACTACAGAAGTTTCTTCTCGAAGCGCCTCAGCGATTTTTAAATCGTATGCAGAAATATCAAT  
TTGAAGCAGTGGTTGGCCACAAAAATCAAATGAAATGAATAAGCTCCAGCCAGGACGATG  
TATGCATGATAATGATATGAATAGTTTCAATCAATGCTGCAAAAGCTTTATTTTCACATTTTT  
TCAGTCTCGATAATATTA AAAACATTTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGCTTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTCT  
TCATGCCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATA  
TTTTTTTTTTCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTTAAGATTCAAGCATTTGAAAGAATTTCCCTAGCCTCTTCCCTTT  
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCCCTCATATTTTCTCCCTTTTATAGTCTTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAAATTTATGCTTTCATATATCCTTGGTCCAGAGATGTTTAGACAAAT  
TTTAGGCTCAAAAATTAAGACTAACACAGGAAAAGGAACGTACTGGCTATTACATAAGAAA  
CAATGGACCCACAGAGAAGAA

## **FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEIILLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVBETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

**0907**

CGCGCGCGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCACGACGAG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCACGCCGCCCGGGGCG  
AGGATGACCAAGGCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCCGTGTTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCGGGGCGGACAGGGACAGGGAGCTCAGC  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACCTCGAGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCTGCAACCACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCAGACA  
CGTGCAACAACGCCAGCGCGCACTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCCCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCGACAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCATGCTGCGGCTGTACGCCAACCAACACAGCCTGCCCGCCTCGCGCG  
GCGAGGCCTTCCGCGCTGGCTCAAGGTGTCTTTCGCCAACCTTATCCAGTACCTGTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGCGCAGGTGTACCGCCTTGCCTA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCCGCG  
AGCTGCTGCAGCTACTCCAGGTGGACCGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACCTCTACGAGGCGGACTTGTGTTCTCTTCGCTACGCCAACAGGCCGAAAACCTCCTCC  
GAGACTGGAAGCTTTCGCGTGTCTTTTCTTCGCTGCTACCGACTTGGACGACGCGCACTCC  
AGTTTTTTTTATGACCTACGATTTTGGAACCTGGGCTTCTGTTCCTCACTCCACTCGCTCTATCC  
ATTGAGTACTGTATCGATAATGTTTTTTAAGATTAAATATATTTCAAGGTATTTAATACGA

## **FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSPHTGPPLPTGPDRELT  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESSVRGYDWSFRDARRSPDQGRQQAER  
RSVLRGFCANSSLAPPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS  
GSLLRGAPYRDLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

#### **TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

## **FIGURE 195**

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGGCGGGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCAG  
CCACTGGGCCGATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGTGCAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATT  
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCAACCTGCAGGTTCCCAT  
AAAAACGATTTCAGCC

## **FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCTGGGCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGAGAGTCAACTTGCAGCT  
GTGGAATGTCACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGTTGTTAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCAGAAAGCCAGGCAGCAGCCCGAGA  
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

[illegible]

&lt;subunit 1 of 1, 180 aa, 1 stop

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGHQVPLDLVSRMKPYARMEEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHPSRIPVDLPEARCLCL  
GCVNPFTMOEDRSMVSVPVFSQVPRRRLCPPPPRTGPCRORAVMETIAGVGCTCIF

Signal peptide:

N-glycosylation site.

Homologous region to IL-17

amino acids 96-180.



## **FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQTDSWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISFCFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEDEEEEDNLAAGVDEERSEANDQGPPGEDGVTRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187



## **FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIEKSCYLFMSLSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

# FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA  
 CACAGGCTGGAGTGCAGTGTGTGATCTTGGCTCATCGTAACTCCAACCTCCGGGTCTCAAGTGATTCATCATGCC  
 TCGCCTCCCGAGTAGCTGGGATTACAGTGGTGCATCTTCAAGAGTACTCCGTCGAGGAAAATGACTCCCGAG  
 TCGCTGCTGCACAGCAGACTGTTCCTGCTGACTCTGCTCTTCTGGTGCAGAGTGCACAGCGAGGGCCACAGG  
 GAAGACTTTCGCTCTGTGCAGCCAGCGGAACACAGACACAGGAGCAGCCTCCATCTACCAACACACACAGACTCG  
 CGCATCTTCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTCTCCCTGACGCCACCTGCTTCCCGA  
 TCCTTCCCTGACCCAGGGGCCCTTACCACCTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC  
 TATGGCAAGCGTGACTTCTTGTCTGAGTGACAAAGCCTCTAGCCTCTGTGCTTCCAGCACAGGAGGAGCGCTG  
 GCTCAGGGCCCGCCGCTGTTAGCCACTTCTGTCACTCTCGTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC  
 GCCAGCTTCACCTTCTCTTCCACAGTCTCTCCCCACAGCGCCCTCACAATGCCCTCGGTGGACATGTGCGAGCTC  
 AAAAGGGACCTCCAGCTGCTCAGCCAGTCTCTGAAGCATCCCAAGAGGCCCTCAAGGAGGCCCTCGCTGCCCTCC  
 GCCAGCCAGCAGTTCGACAGCCTGGAGTCGAACCTGACCTCTGTGAGATTCTAGGGGACATGGTGTCTTCGAG  
 GAGGACCGGATCAAGCCACGGTGTGGAAGCTCCAGCCACAGCGGCCCTCCAGGACCTGCATCTCACTCCCGCG  
 CAGGAGGAGGAGCAGAGCAGATCATGGAGTACTCGGTGCTGCTGCCCTCGAACACTCTTCCAGAGGACGAAAGGC  
 CGGACGCGGGGAGCTGAGAAGAGACTCTCTCGTGGGACTTCAGCAGCCAAAGCCCTGTTCCAGGACAGAAGATTCC  
 AGCCAAGTCTCGGTGAGAAGGCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACTCAGCGAGCCGCTG  
 GTGCTCACTTTCAGCACCAGCTACAGCOGAAGAATTGTACTCTGCAATTGTGTCTTGGGTGAAGACCCCA  
 TTGAGAGCCCGGGGCTATGGAGAGCTGCTGGGTGTGAGACCCGTGAGGAGAGAAACCAAATCCTGCTTCTGCG  
 AACCACTTGACCTACTTTGTAGTGCTGTAGTGTCTCTCGTGGAGGTGAGCCGCTGCACAACTACTTCTGCTGAGC  
 CTCTCTCTCAGTGTGGGCTGTGCTGCTCTGCGCTGGCTGCTTGTACCAATTGGCGCTCACTCTGTCTCGAGG  
 GTGCGCCCTGCGCTGAGGAGGAAACCTCGGACTACACCATCAAGGTGCACATGAACCTGCTGTGGCCGCTCTTC  
 CTGCTGGACAGCAGCTTCTGCTCAGCGAGCCGTTGCCCTGACAGGCTCTGAGGCTTGGCTGCCGAGCGATGCC  
 ATCTTCTGCACTTCTCCCTGCTCACTGCTCTTCTGGATGGGCCCTCGAGGGGTACAACTCTTACCGACTCTGTG  
 GTGAGGCTCTTTGGACCTATGTCTCCCTGGCTACTACTCAAGCTGAGCGCATGGCTGGGCTCTCCCATCTTT  
 CTGCTGACGCTGGTGGGCTGTTGGATGTGGACAATATGGCCCATCATCTTGGCTGCTCATAGGACTCCAGAG  
 GCGCTCTACTTACCCTTCCATCTGGATCGGGACTCCCTGGTCAGCTACATCAACCACTGGGCCCTCTTTCAGC  
 CTGCTGTTCTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGAGATCTCGGGCTGCCGCCCAACCCCAA  
 AAGTGGTCACATGTGTCACATGTGTGGGCTCAGCCTGGTCTTGGCTGCCCTGGGCTGTGATCTTCTTCTCC  
 TTTGCTTCTGACACCTCTCCAGCTTGTGCTCTTACTCTTTTCAAGTATCATCACTCTCTCCAGGCTTCTCTATC  
 TCTATCTGTACTGCTTCACTGGCTGAGGCCCGGGGTGGCCCTCCCTCTGAAGAGCACTCAGACAGCGCC  
 AGGCTCCCCATCAGCTCGGGCAGCACCCTGCTCAGCGCCATCTAGGCCTCCAGCCACCTGCCATGTGTGAAG  
 CAGAGATGGGCGCTCTGTCGACACTGCTGTGGCCCCGAGCAGGCCCAGCCCCAGGCGAGTCAAGCCGACAGAT  
 TTGGAAGGCCCAAAGCAGCATGTGAGAGATGGCGGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTG  
 GCCTTGGGGACTACTCGGCTCTCATCAGCTCCACAGGGAATCAGAAGTGGCGCGCCGACATGCTGCCATAGGTA  
 TCTTCCACATCTGTCCCAACCCAGCTGGAGGCTGGTCTCTCTTACAACCTCCGGCCAGCCCTCATTTGCTGGG  
 GGCCAGGCTTGGATCTTGAAGGTCTGGCACTCTCTTAATCTGTGCCCTGCTGGGACAGAAATGTGGCTCCA  
 GTTGTCTGTCTCTCGTGGTCACTCGAGGGCACTCTGATCTCTGTCTTTAACTCAGGTGGCAGCCAGGG  
 CGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCCCTGCGGAGGAGAGGGCCCTTGCACAGGAGCAGCAGCAG  
 AGCTCGCTACCTCTGAGGCCAGGGCCCTCTGCTCCCTCAGCGCCGAGTCTCTCCCTCATCTTCCCTGGGGTTC  
 TCTCTCTCTCCAGGGCTCTTGTCTCTCTGTTCAAGCTGGGGGTCCCGGATCCAATGCTGTTTGTGGGGA  
 GTGGTCTCAGGAGCTGCTGGTGTCTGCTGTAATGTTGTCTACTGCAAGCCTCGGCTCGCCCTGAGCCA  
 GCTCGGATACGATGCGTGGGCTGGGCTAGTCTCCCTGTGCTCATCTGGGCCCTTTGATGAGCTGCATTTGCCCTTG  
 CTCACCTGACCAAGCACAGCCTCAGAGGGGCCCTCAGCCTCTCTGAGGCCCTCTTGTGGCAAGAACTGTGGGA  
 CCATGCCACTGCTGCTGTTTCCATCCCACTCAGGAGTCTGAGCTGACCTCTCTGTGACACTGGGCTCA  
 GAGCTGCACTCTCTTAAGAGGTTCTCTCAAGCCCAATAGCTCAGCGGCCCTCGGCGGCCCATCATGTT  
 TAAATTCTGTCCAAACAAACACACAGGGTAGATTGCTGGCCTGTTGTAGTGGTAGGACACAGATGACCGAGCTG  
 GTCACTCTCTCGCAACATTCAGTCTGGTATGTGAGGCGGTGGTGAAGCAAGACTCTGAGAGTCTCGAGGACA  
 GGGAGCCATCATCTCTGCTGGGAATCTGGAAGACTTCTCGAGGAGTCAAGCTTCAATCTTGACTTGAAGAT  
 GGGAGGATGTTCTTTTACGTACCAATTTCTTTGTCTTTTGATATTAAGAGAGTACATGTTCTATTGTAGAGA  
 ATTTTGAAGACTGTAGAAGAGAAATCAAGAAGAAAAATAAAATCAGCTGTGTAATCGCCTAGCAAAAAA  
 AA

0978191.101501

## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MT PQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTDRLRISIENSE  
EALT VHAPFPAAH PASRSFPDPRGLYHFC LYWNRHAGRLHLLY GKRD FLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNI SLPSAASF TFSFHSPPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTPVVLT FQHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRR  
TQTSCFCNHLTYFAVL MVSSVEVD AVHKHYLSLLSYVGC VVSALACLVTIAAYLC SRVPLPC  
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY  
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG  
LPWALIFFSFASGT FQLVVL YLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSNSDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

## **FIGURE 205**

TGCCTGGCCTGCCTTGTCACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNCAAGTGCACATGAACCTGCTGCTGGCCGCTTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCTTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTTCTGTTCAACATGG



## FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRDTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

**Signal sequence:**

amino acids 1-14

6  
5  
4  
3  
2  
1  
1  
2  
3  
4  
5  
6

# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACACGACCTCTACATTCATTTTGGGAAGA  
 AGACTAAAAATGGTGTTTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCTCTTTTAAACATAATCTCTAAATTTCC  
 AAATCTCTTGGGGCTAGATGTTTCTTAAACTCTGCCCTGIGATGTCACTCTGGATGTTTCCAAAGAACCTATGTG  
 ATCTGGAGCTGCACAGACAGCAATTTGACAGAAATTCCTGGAGGTATTTCCCAAGAACACACGAACTCACCTC  
 ACCATTAACACATACACAGACATCTCCACGCGTCTTTCCACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA  
 TGCACTGTGTACCTATTCCACTGGGGTCAAAAAACCAATGTGCATCAAGAGGCTGCAGATTAACACCGAAGGC  
 TTTAGTGGACTCACTTATTTAAATCCCTTACCTGGATGGAACACGAGTACTAGAGATACCGCAGGCGCTCCCG  
 CTTAGCTTCAGACTCTTCAGCCCTTGGGGCCAAACACATCTTTCCATCAGAAAAAGAGAATCTAACAGAACTGGCC  
 AACATAGAAATACTCTACCTGGGCGAAAACTGTTATTTATCGAAATCTTGTATGTTTTCATATTTCAATAGAGAAA  
 GATGCGCTTCTAAACTTGACAAAGTTTAAAGTGCTCTCCCTGAAAGATAACAAATGTGCAGAGCGCTCCCTACTGTT  
 TTGCCATCTACTTTAAACAGAACTATATCTCTACAAACAAATGATGTGCAAAATCCAAGAGATGATTTTAAATAAC  
 CTCACCAAAATTACAAATCTTGACCTAAGTGGAATTTGCCCTCGTGTATATAATGCCCATTTTCTGTGCGCGG  
 TGTAAAAATAATCTCCCTACAGATCCCTGTAAATGCTTTTGTATGCGCTGACAGAAATTAAGAGTTTACGTCTA  
 CACAGTAACCTCTTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGCC  
 CAAAATCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCGAGCTCATCCAATTTGGATCTG  
 TCTTTCAATTTTGAACCTTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
 AAAATCTCGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAAACCTCTCGCCATTACATAATCTTCAA  
 AATCTTGAAGTCTTGATCTTGGCACTAACTTTATAAAAAATGTCTAACCTCAGCATGTTTAAACAAATTTAAAGA  
 CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAGGTGAAGTTGGCTTCTGCTCAAAT  
 GCCAGAACTCTGTAGAAAGTTATGAACCCAGGCTCTGGAAACAAATTACATATTTAGATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTCTTTCATGTCTGTAAATGAAGCTGCTACAAAGTATGGGACAGAC  
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAGACTCTTTCTTCCCAAAATGCTG  
 AATCTGTGAGGAAATCTCATTTAGCCAACTCTTAATGGCAGTGAATTCACAACTTTAGCAGAGCTGAGATATTTG  
 GACTTCTCCAACAAACCGCTTGATTTACTCCATTCACACAGCATTTGAAGAGCTTCAACAACTGGAAGTTCTGGAT  
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTAATCATATGCTTAACTTTTCAACAGAACTTAAAGGT  
 CTGCAAGAACTGATGATGAACAGCAATGACATCTCTTCTCCACAGCAGGACCTGGAGAGTGAGTCTCTGAT  
 ACTCTGGAATTCAGAGGAATCTAGATGTTTATGAGAGGAAGGTGATACAGATATCTCAATATTTTCAAG  
 AATCTCTAAAATAGAGGAATAGACATCTCTAAAAATTCCTAACTTTCTGAGTTCTGGAGTTTGTGATGT  
 ATGCCCTCCAAATCTAAGAAATCTCTCTTTGGCCAAAAATGGGCTCAATCTTCTGATTTGGAAGAACCTCAGTGT  
 TPAAGAACTCGAAATCTTGGACCTCAGCCACAAACCACTGACCATCTGCTCGAGAGATTAACAACTGTTCC  
 AGAAGCTCTAAGAAATCTGATTTCTAAGAATAATCAATCAGGAGTCTGACAGAGATTTTCTACAGAGTGCCTTC  
 CAGTTGCGATATCTGATCTCAGCTCAGCTCAAAATAAATCAGATGATCCCAAGACCTGCTTCCAGAAATGTCTCC  
 AACATCTGAAGATGTTGCTTTTGGCATCATAACTCGTCTTGTGACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
 GTTAACCATCGGAGGTGACTATCTTACCTGCGCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
 CAAAGTGTGATCTCCTGGATCTGTACCTGTGAGTTAGATCTGACTAACCTGATCTGTTCTCACTTCCATA  
 TCTGTATCTCTTCTCATGTGGTATGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGTATATTTACAT  
 TTCTGTAAGCCAGATAAAGGGGTATCAGCGTCTAAATACACAGACTGTGCTATGATGCTTTTATTTGTGTAT  
 GACACTAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGTGTGGCCAACTGGAAGACCCAGAGAGAAA  
 CATTTTAAATTTATGCTCGAGGAAAGGGGACTGGTTACACAGGCGAGCGAGTTCTGGAACAACTTTCCACAGAGCA  
 CAGCTTAGCAAAAAAGACAGTGTTTTGTGATGACAGACAGATGTGCAAGACTGAAAAATTTTAAAGTAGCATTTTAC  
 TTGTCCCATCAGAGCTCATGGATGAAAAAGTTGATGTGATATCTTGTGATATTTCTTGAGAGGCTTTTCAAGAG  
 TCCAGATTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTTCTGCTTGTGAGTGGCCACAAACCCGACAGCTCAC  
 CCATATTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAAATCATGTGCGCTATATGTCAGGTGTTCAAGGAA  
 ACGGTCTAGCCCTTCTTTCGAAAAACAACTGCTAGTTTACCAAGGAGAGGCTCGC

0978191-101503

## **FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRDLHVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIIRKENLTLANIEILYLQNCYYR  
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL  
NQLQIILDLSGNCPRCYNAPFFCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF  
KNINKLQELDSLQNFLAKEIGDAKFLHFLPSLIQLDLSFNLFQVYRASMNLSQAFSSLSLSL  
KILIRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMPKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFRKNKEASFMSVNESCYKYGQ  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEEHLHKLLEVLDISSNSHYFQSEGITHTMLNFTKNLKVQLKMMNDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPNKLKNSL  
AKNGLKSFWSKKLQCLKNLETLDSLHNQLTTPERLSNCSRLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHRNRLCTCDAVWFVWWVNHTVETIP  
YLATDVTCVGPAGHKQSVISLDLYTCELDLTNLILFSLSSISVSFLMVMMTASHLYFDWVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPQGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYPWQCLKNALATDNHVAYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

# FIGURE 210

GGGTACCATTTCTGCGCTGCTGCAAGTTTACGGAATGAAAAATTAGAACAACAGAAACATGGGAAACATGTTCTCTTC  
AGTCGTCAATGCTGACGATGCAATTTTCTGCTAATATCTGGTTCTCTGTGAGTTTATGCGCGGAAGAAAAATTTCTTA  
GAGCTATCTTGTGTGATGAAAAAGGCAAAATGACTCAGTTATTTGCGAGGTGACGCAATCGTCGACTACAGGAAG  
TTCCCCAAACGCTGGGCAAAATATGTGACAGAACTAGACCTGTCTGTAATTTTCATACACACATAAGCAATGAAT  
CAATTTACAGGGCTGCAAAATTTCTCAATAAAATAATCTAAACCCACACCCCAATGTACAGCAGCAGGAACGGAAATC  
CTGCTATACAAATCAAAATGGCTTGAATATCACAGACGGGGCAITTCCTAACCTAAAAAACCTAAGGGAGTTTACTGC  
TTGAGAGCAACACAGTTACCCCAAAATACCCCTCTGGTTTGCCAGAGCTCTTTGACAGAACTTAGTCTAAATTCAAAAACA  
ATATATACACATAAATCAAGAGAGGCGATTCAAGACTTATAAATCTGAAAAATCTCTATTGGCTGGAACTGCT  
ATTTTAAACAAAGTTTGGCAGAAAACTAAACATAGAAGATGGAATTTTGAACAGCTGACAAAATTTGGAGATTTGCTAT  
CACTATCTTTCAATTCTCTTTCAACGTCGCCAACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCGAGCAACA  
CCAGATCAAAATACATTAGTGAAGAGAGATTCAAGGGATGATAAATTTAACATTACTAGATTTAAGCGGGAAT  
GTCCGAGGTGCTTCAATGCCCAATTTCCATGCGTGCCTTTGTGATGGTGGTCTTCAATTAATATAGATCGTTTGT  
CTTTTCAAACTTGACCCCACTTCGATACCTTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT  
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCACATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
TTTAAACGATGCTGCCCGCTTAGAAAACTTGAATCTGTCTTTAACTATATAAGGGGAGTTATCCACAGCATA  
TTAATATTTCCAGAAAATCTCTCAAACTTTTGTCTACCGGCAATTGCATTTAAGAGGTTATGTGTTCCAGGAAC  
TCAGAGAAGATGATTTTCACTCCCTGATGCGAGCTTCAAACTTATCGACTATCAACTTTGGGTATTAATTTTATTA  
AGCAAAATCGATTTCAAACTTTTCCAAAATTTCTCCAACTCGAAATTTACTTTGTCAGAAAAAGAAATCAC  
CGCTTGTGTAAGATACCCGGCAGAGATTATGCAATAGTTCTCTTTTCAAGCTCATATCCGGAACAGACGCTCAA  
CAGATTTTGAGTTTGACCCCAATTCGAACTTTTCACTTACCCTGCTTTTAAATAAGCCCAATGTGCTGCTT  
ATGAAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAITGGGCGCAACCAATTTTGAATATTTCTCTGACA  
TGCTGCTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTTAAGTGGAACTGAATTTTCAGCCATTTCTCTGAT  
TCAAAATTTTGATTTTGAACAACAATAGACTAGACTTTGATAATGCTAGTGCCTTCTACTGAATTTGCTCCGACTGG  
AAGTTCTAGATCTCAGCTATAAATTCACATAATTCAGAAATAGCAGGCTGAACACATCATAGAATTTATCAAA  
ATTTTCAAAATCTAAAGTTTAAATCTTGAGCCACAACAACATTTATCTTTTGAACAGATAAGTATAAATCTGAAA  
GCAAGTCCCTGGTAGAATTAAGTTTTCAGTGGCAATCGCTTGACATTTTGGAGATGATGATGACAACAGGTATA  
TCTCCATTTTCAAGGCTCTCAGAATCTGACACGCTCGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAT  
AAGCAATCTTAAATTTGCCAGCGCTCTCACTGAATCAATATAAGTATAATTTGAATTTTAACTGGA  
CTTATCTCAGACGATTTTCTCTGCTCTGAGTGTGCTGACTTACGTGGAACAAAATCTACTCTTTTAACTGATAGC  
TATCTGACTTTAGATTTTCTCTCTGCGACACTGCTGCTGAGCTATAACGAGATTTCCCACTACCTCTGCTGCTTCT  
TTTCTGAAGTCAGTAGTCTGAGACGCTCGAATTTAAGTTTCAATCTGCTAAAAACATCAACAATCCGCACTTG  
AACTAAGACCCACCAAAATATCTATGTTGGAACCTACCGGAAACCCCTTTGAATGCACTGTGACATTTGGAG  
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCGAGACTGGTAGATGTCAITTTGCGCAGTCTCTG  
GGATCAAAAGGGGAAGAGTATGTGAGTCTGGAGCTAACAACTTGTGTTTCAGAGTGCATCTGAGTATATAT  
TTTTCTCACGTTTCTTATCACCACATGGTTATGTTGGCTGCCCTGGCTCAGCAATTTGTTTACTCGGAGATGTT  
GTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGCTCTTTTCCACATCCCAATCTTCTATGATG  
CTTACTTTCTTATGACCAAAAGATGCTCTGTTACTGACTGCGGTGATAAATGAGTCTGCGCTACCACTTTGAAG  
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTTGGGACCCGGGATTTGGCCATCATCGACAACT  
TCATGACAGACATCAACCAAGACAGAAAAAGTATTTGTTTATAACCAAAAAATATGCAAAAAGCTGGAATTTTA  
AAAACGCTTTTACTTTGGCTTTGACAGGCTAATGGATGAGAACATGGATGTGATATATATTTTCTGCTGGAGC  
CAGTGTGTCAGCATTTCTCAGATTTTGAAGCTACCGCAGCGGATCTGTAAGAGTCTCATCTCCAGTGGCTGACA  
ACCGAAGGCGACAGAGGCTGTTTGTGGCAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACA  
ATATGTATGTGCAATTCATTAAGCAATACTAACTGAGCTAAGTCAATGATTTTCCGCCCAATAAAGAGTGCAAG  
GAATGACATTTCTGATTTAGTATCTATTTGCTATGTAACAAATTATCCCAAACTTAGTGGTTTAAACACAACA  
TTTGTGCGCCCACTGTTTGGGGCTCAGGAGTCCAGGCCAGCATAAATCGGCTCTCTGCTCAGGGTGTCTCAG  
AGGCTCGAATGTAGGTGTTCACACAGACATAGGCACTACTGGGGCTCACACTCATGTGGTGTGTTTCTGGATTCA  
ATCTCTCTGGGCTATTGGCCAAAGGCTATACATCATGTAAGCACTGCGAGCTCTCCCAAGGCAAGTGTCTCTC  
ATCAGAGCTAGCAAAAAGAGAGGTTGTCTAGCAAGATGAAGTCACAACTTTTGTGAATCGAATCAAAAAGTAT  
ATCTCATCACTTTGGCCATATTTCTATTTGTTAGAAGTAAACACAGGCTCCACAGCTCCATGGGAGTGACACC  
TCAGTCAGGGAAGAACAGCTGGAAGACCAAGATGGTGAAGTCTGATGCTCAGTTGGTCACTCAACTATTTCCCT  
TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTAATCTGAGGACAGGATCACTGTGGACC  
ATCTTAGAGCTGCACTAACACATCTTCTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGTGCTTAAT  
TTAAGCTGTGTTTATATTTTATCATATCTATGGCTACATGGTTATATTAATGTGCTGTGCTGTGCTGTTTAT  
TTCAGTGTCTTTTCAAAATTTTCTGTAACTTTGACTTCTAAGGTTTGAATGCCATTTAAGAACTGAGATGG  
ATAGCTTTTAAAGCATTTTACTTCTTACCATTTTTTAAAGTATGCAAGTATGAAGCTTTTGGCTTATATA  
TTGTTAATTTGCCATGCTGTAATCTTAAATGAATGAATAAAATGTTTCATTTTCAAAAAA

## **FIGURE 211**

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLHNPNVQHQNGNPGIQSNGLNITDGAFNLN  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLDDLSGNCPRCFNAPFPVPCDGGASINIDRFQNLTLQLRYLNLSSLSLRKINAAWFKNM  
PHLKVLDELFEYNLVGEIVSGAFLTMLPRLEILDLSFNKSYKSYQPHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDDEFDPHSNFYHFTRLPIKQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTELHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRI SHLPSGFLSEVSSLKHLDL  
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSELELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFVIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELEHYHLEESRDKNVLLCLEERDWDPLGAIID  
NLMQSIHQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLFWQTLRNVLVTENDSRYNM MYVDSIKQY

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 826-848

## FIGURE 212

CCAGGTCCAAC TGCACCTCG GTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCTTCAGGGCGCCAGTGGGCTGAGGCCACGCTGGG  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGG  
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCTGTCCGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCTCTCA  
CCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCTGCCAGGCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCTTGGGGCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGTGCCGTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGTGTGCCAGTGTGTGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCACCTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCATCTCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTCTCTG  
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCC  
TTCTCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCCCCGAG  
GCTGGTGGTGGGCCCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAAATAAAATGAAACGTGA  
AAAGGGCGGCCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATTCAGCTTATAATGTTACAAAT

## 09761-10100

Signal sequence:

1-19

0962131363

[illegible]

## FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQFFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKLLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

## FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCACACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTCTGTGAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCACTGTCTAGGAGGGGCGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG  
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCTTGAGGAGCAGCT  
GGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCACGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCTCCCTTCTCTGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTAATCCACCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGTGAGGCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTG

[illegible]

Signal sequence:

1-19

AGTTGGCCACAGCTGGTTTGGGCGCCGACCACTGGGGCCGCTTGTCAAGAGAGACAGCCTCCGGGCGGGGAG  
GACAAGTCGCTGCCAACTTTGGGCTCGACAGTGATTCCTGGAGACGCTGGTTCCTTGGCCTGACGTCGCGCCCG  
AGTTGGGTCCTCGGTGTTTCAGCGCCGCTCCGCCCTCTCTGGTCTCCCTTCTCCCGCTGGGCGCGTTTATCCGAGAG  
AGATTTCCTCCAGGCTAGCAATTGGACCTTTTGTATGATGTTTGACCCAGGCGAGGATAGCAGGCAACGTAAG  
TCCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTGTGTAATCGCAAAACCACTTTGGAGCAGGAATCCAAATCA  
TGTCTGTGATGGTGGTGAAGAAAGAGGTGACA CGAAATGGGAGAACATCCCAGGACAGGAACCACTTTGCTGT  
ATGGCCGCTACATAGTGGCCGGGATAAAGGACATTTCTACCTGACCCCTTTCTCTATCTGGGACATGTGTACAC  
TCTTTCTTGGCCTTTTGAATGGCGCTCACTGCTGCTTTCAGCTGTCTCTCGTCACTCCCTGTATTTCTTGGCCTACGCTCT  
TCTCTTTCTCATGGCTACACTGTTTGGAGCAACAGCTTCAGTGCACCTGGAGTGATTTCTCGGGCGCTACCAAGT  
AAGCAGCTTTTCATAGAAATGGAGATGAAGCTACAACATGGTGGCGGTGGCCCCAGGGCCAGGCACACCCGCTGTGTA  
TCAAGAATTTCGATGACATAAACACAGATGTGTAACTGAAATCAATGTGTACATGCAGAATCTTCGCGCTCTCCC  
GGGCTCCCTCAATTCAGCAGCTCTGTACACACTGTGTGGAGCGCTCTGACACATCACTGCCCTGGGTGGGGAATTTGT  
TGTGAAGAAAGAAATACCGCTACTTCTACCTCTTCACTCTTCTCTCTCTCTCAACTATATGTCTTCTGCTCT  
TCAACATCGTCTATGTGGGCTCAAACTTTGAATAATGGCTCTTGGAGACATGTGAAGAAATCTCTGGAACCT  
TCTCAGAAGCTCTCAATTTGCTTTCTTACACTCTGGTGGCTGTGGGAGTACTGGATTTTCACTATTCTCTGGT  
CTCTACACCAACCAACCAATGAGACATGAAGGATCTGAGCAGAGGAAGAATCGGTGTCGCAATCCCAACGCC  
ATGGCTATATTGTGGAAGACTGTGTGATGTGAGTGTGTGGCCCTTGCCCCCAAGCTGTCTGGATCGAAGGGTGA  
TTTGGCCACTGGAGAAAGTGAAGTCAAGGCTCCAGATCTCAAGAGACAGTACAGCCTCTTTCGACACAGCC  
GAGCCCCGACCAACCACTGAACTCAAAATGAGATCGCGAGAGCAGCAGCACTCCCGAAGAGATGCCACTCTCAG  
AGCCCCGACGACGCCACACAGGCGGAGCTGAAGCTGAGAACTAGCCTATCTATGGAAGAGCTTTTGTGTTGT  
TATTTAGGCTATGAGAGATTTTCAGTGTGAGAGTGAACCTTGAGACAGAGCAAGTAAGCTGCTCCCTTTTAACCT  
GTATTTCTTTTGGTCTTTTATGATCCCACTGTGCACATGGAATTTTCTGTGTCAGAGCTTTTAAATTTTGAACCT  
CAAGGCAAGTGGCAGAGATGTGAGTCACTCTGATATGCGAAATAATGGGTCTCTTGGGCCCTGGCCTAGTCTCT  
CCATGGCTCAGGCCACAGGCTCGCTTGGACCCCTCTCTCTCCAGCTCCAGCCCTCTGCTCTGGGGTCACT  
TGGTCTCTATTCTGGGGCTAAAGATTTTGTAGAATGGCTCAATCTCTCCCAAGCTGCTGCACTGCTGAGTCCAGA  
GGCAGTCAACAGAGCACTCTGCGCCAGGGATCTCAACTGGGTTCTGGGGTCTTCAAGACTGAAGAGGAGGAGAG  
TGGGGTCAGAAGATTTCTCTCGCCACCAAGTGCAGCACTGCCCACAAATCTTTTGAAGATGCCAGAGTATGCT  
TCCACTTTGTGTATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTTTCTTTTCTTTGACTCTGCTGCGCATAGG  
CAGGAATCGGAGTAAATAAGTCTGACCTCTTGCTCATTTCTTTCTCTCAGAGGAAGCCGAGTGTCTCACTTAAC  
ACTATCCCTCAGACTCTCTGTGTAGGCTCTGAGAGGCCCTGAATGCAACATGGGAATAACAGGCAACAGAGAG  
GCTCTCTCTCTCTCTCTCTCCCGGATGTACCTCAAAAATAAAAAAATGCTAACAGGTTCTCTCCATTAAAGCT  
CGGCTGAGTGGGAGAAACCGCAGCTGTGCTCTCTCGGGTAATCACTCCCTAAGGCTCTCGGCCACCTCTGGCT  
ATGGTAAACCACTGGGGCGTCTCTCCACAGCCCGGCTCTCTCAGACACTCTCAGCGGCAAGTCCGACAGCACT  
CACCTCGGGGTGGGCTGTGGCCGCCAGTCAAGCTGTGTCAGGACCTGTCTATTTCAGGGAAGAGTAATGTAT  
ATTATATGTGCTATATTTCTCTAGAGCACTGTGTTTCTCTTTTAAACCGAGGCTCTGTCTGGTGAACCTTA  
CGGTTGGGGAGTGTAAACCGGAAGTTTTCATCTATTTGAGGCGGATTAAGCTGTGTCTATGCA

## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLEKETPGTVLEVLI CFFTLWSVVGLTGFTF  
LVALNQTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPEPEPPQEAAAEAK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

## **FIGURE 220**

AAAACCCGTGATTTTTTACAATGCAAAATAGACAATNANCCTGGAGGTCCTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCTCACAACTATGTCTTCGCCTTCA  
ACATCGT

09978191.101501

090701-1

GTGTGTCTCTTCAGCAAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAAGAAAGAAAGAA  
AAAAAATCATGAAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCATTATT  
GACAAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCTTGGATCCTCGCGTGGTCTCTCTGAGCAACACCACCAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGACAAC  
CACCACAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTC  
TTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTTCAGGCATCACCCGGGAGCAGTACAGGGACTACGAGTGCAGTGCCCTC  
CAATGACGTGGCCGCGCCGCTGGTACCGGAGGTAAAGGTCACCGTGAACATGCCATTACA  
TTTCAGAAGCCAAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAACACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACACACTTGGTGGCCCTCCAACAAGCTGGGGCCACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGGAAAGAGTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGAGCCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATCTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCATTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

## **FIGURE 222**

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIETQNVVDVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASANDVAAFVVRVKVTVNYPYI SEAKGTGVPVGQKGTLCCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHGTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLF

**Signal peptide:**

amino acids 1-28

**THE UNIVERSITY OF CHICAGO**

GAAAAAAATCATGAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAGCTATGGACAACGTGACGCTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCTCTTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCACAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCCAGAG

☐ 1. ☐ 2. ☐ 3. ☐ 4. ☐ 5. ☐ 6. ☐ 7. ☐ 8. ☐ 9. ☐ 10. ☐ 11. ☐ 12. ☐ 13. ☐ 14. ☐ 15. ☐ 16. ☐ 17. ☐ 18. ☐ 19. ☐ 20. ☐ 21. ☐ 22. ☐ 23. ☐ 24. ☐ 25. ☐ 26. ☐ 27. ☐ 28. ☐ 29. ☐ 30. ☐ 31. ☐ 32. ☐ 33. ☐ 34. ☐ 35. ☐ 36. ☐ 37. ☐ 38. ☐ 39. ☐ 40. ☐ 41. ☐ 42. ☐ 43. ☐ 44. ☐ 45. ☐ 46. ☐ 47. ☐ 48. ☐ 49. ☐ 50. ☐ 51. ☐ 52. ☐ 53. ☐ 54. ☐ 55. ☐ 56. ☐ 57. ☐ 58. ☐ 59. ☐ 60. ☐ 61. ☐ 62. ☐ 63. ☐ 64. ☐ 65. ☐ 66. ☐ 67. ☐ 68. ☐ 69. ☐ 70. ☐ 71. ☐ 72. ☐ 73. ☐ 74. ☐ 75. ☐ 76. ☐ 77. ☐ 78. ☐ 79. ☐ 80. ☐ 81. ☐ 82. ☐ 83. ☐ 84. ☐ 85. ☐ 86. ☐ 87. ☐ 88. ☐ 89. ☐ 90. ☐ 91. ☐ 92. ☐ 93. ☐ 94. ☐ 95. ☐ 96. ☐ 97. ☐ 98. ☐ 99. ☐ 100. ☐ 101. ☐ 102. ☐ 103. ☐ 104. ☐ 105. ☐ 106. ☐ 107. ☐ 108. ☐ 109. ☐ 110. ☐ 111. ☐ 112. ☐ 113. ☐ 114. ☐ 115. ☐ 116. ☐ 117. ☐ 118. ☐ 119. ☐ 120. ☐ 121. ☐ 122. ☐ 123. ☐ 124. ☐ 125. ☐ 126. ☐ 127. ☐ 128. ☐ 129. ☐ 130. ☐ 131. ☐ 132. ☐ 133. ☐ 134. ☐ 135. ☐ 136. ☐ 137. ☐ 138. ☐ 139. ☐ 140. ☐ 141. ☐ 142. ☐ 143. ☐ 144. ☐ 145. ☐ 146. ☐ 147. ☐ 148. ☐ 149. ☐ 150. ☐ 151. ☐ 152. ☐ 153. ☐ 154. ☐ 155. ☐ 156. ☐ 157. ☐ 158. ☐ 159. ☐ 160. ☐ 161. ☐ 162. ☐ 163. ☐ 164. ☐ 165. ☐ 166. ☐ 167. ☐ 168. ☐ 169. ☐ 170. ☐ 171. ☐ 172. ☐ 173. ☐ 174. ☐ 175. ☐ 176. ☐ 177. ☐ 178. ☐ 179. ☐ 180. ☐ 181. ☐ 182. ☐ 183. ☐ 184. ☐ 185. ☐ 186. ☐ 187. ☐ 188. ☐ 189. ☐ 190. ☐ 191. ☐ 192. ☐ 193. ☐ 194. ☐ 195. ☐ 196. ☐ 197. ☐ 198. ☐ 199. ☐ 200. ☐ 201. ☐ 202. ☐ 203. ☐ 204. ☐ 205. ☐ 206. ☐ 207. ☐ 208. ☐ 209. ☐ 210. ☐ 211. ☐ 212. ☐ 213. ☐ 214. ☐ 215. ☐ 216. ☐ 217. ☐ 218. ☐ 219. ☐ 220. ☐ 221. ☐ 222. ☐ 223. ☐ 224. ☐ 225. ☐ 226. ☐ 227. ☐ 228. ☐ 229. ☐ 230. ☐ 231. ☐ 232. ☐ 233. ☐ 234. ☐ 235. ☐ 236. ☐ 237. ☐ 238. ☐ 239. ☐ 240. ☐ 241. ☐ 242. ☐ 243. ☐ 244. ☐ 245. ☐ 246. ☐ 247. ☐ 248. ☐ 249. ☐ 250. ☐ 251. ☐ 252. ☐ 253. ☐ 254. ☐ 255. ☐ 256. ☐ 257. ☐ 258. ☐ 259. ☐ 260. ☐ 261. ☐ 262. ☐ 263. ☐ 264. ☐ 265. ☐ 266. ☐ 267. ☐ 268. ☐ 269. ☐ 270. ☐ 271. ☐ 272. ☐ 273. ☐ 274. ☐ 275. ☐ 276. ☐ 277. ☐ 278. ☐ 279. ☐ 280. ☐ 281. ☐ 282. ☐ 283. ☐ 284. ☐ 285. ☐ 286. ☐ 287. ☐ 288. ☐ 289. ☐ 290. ☐ 291. ☐ 292. ☐ 293. ☐ 294. ☐ 295. ☐ 296. ☐ 297. ☐ 298. ☐ 299. ☐ 300. ☐ 301. ☐ 302. ☐ 303. ☐ 304. ☐ 305. ☐ 306. ☐ 307. ☐ 308. ☐ 309. ☐ 310. ☐ 311. ☐ 312. ☐ 313. ☐ 314. ☐ 315. ☐ 316. ☐ 317. ☐ 318. ☐ 319. ☐ 320. ☐ 321. ☐ 322. ☐ 323. ☐ 324. ☐ 325. ☐ 326. ☐ 327. ☐ 328. ☐ 329. ☐ 330. ☐ 331. ☐ 332. ☐ 333. ☐ 334. ☐ 335. ☐ 336. ☐ 337. ☐ 338. ☐ 339. ☐ 340. ☐ 341. ☐ 342. ☐ 343. ☐ 344. ☐ 345. ☐ 346. ☐ 347. ☐ 348. ☐ 349. ☐ 350. ☐ 351. ☐ 352. ☐ 353. ☐ 354. ☐ 355. ☐ 356. ☐ 357. ☐ 358. ☐ 359. ☐ 360. ☐ 361. ☐ 362. ☐ 363. ☐ 364. ☐ 365. ☐ 366. ☐ 367. ☐ 368. ☐ 369. ☐ 370. ☐ 371. ☐ 372. ☐ 373. ☐ 374. ☐ 375. ☐ 376. ☐ 377. ☐ 378. ☐ 379. ☐ 380. ☐ 381. ☐ 382.

ATGGCTGTGTAACGGCGGGGCGGGGACGGGACCGGGGCGGGGCGGGGACGCTGGGGAGCCCTGA  
ATACCGCTCGGCGCCATCCACCTGAACGCTGCGCTGGAGAGCTGGGACGCAACGTGGGATTCAG  
AAGGACACAGACAGACGCTTTAGGCTACGCACGACGCTGGAGCTGTGTTAGAGGCTGCTCTTCTACTGTGGCT  
GCATCTCTTCTGSGCTGCTCTGTGGCCCTAGGGGTCCAGTACACAGAGACCCATCCACAGCAGCTGCCCTTACA  
GAGGCTCTGCATTGAGTGGCTGGAAAACTCTGGAGTCCGCTGGACGAGGGGTGAGCCCTCTGTAGAGCTTTTAC  
CAGTTCTCTCTGTGGGGTGGATTCTGGAGAGAACCCCCCTGCGCGATGGGGGTTCTCTGGTGAACACCTTCTCAACAGC  
CTCTGGAGCAAAAACAGGCGCATCTGAAGCACTCTGTGAAAAACACATCTTCAACTCAGCAGTGAAGCTGAG  
GACGACACAGACAGCGCTTCTACTTCTTGCTTACAGCTGGAGCGCATAGAGAGCTGGGGCCAGCCAGCTAGAGA  
GACCTCATGGAAGATTGTTGGTTGGAACATTACGGGGCCCTGGGACAGGACAACTTATGGAGGCTTTGAGA  
CGAGTAGCAGGGACCTACAGGCGACCCCACTTCTACCCGCTTACATCTAGTGGCGCATCTAAGAGTCTTCAACAGC  
AATGTTATTCAGGCTGGACAGCTCTGGGCTCTTTCTGCCCTCTGGGATTACTACTTAAAGAGACTGCCAATGAG  
AAGTGTGCTCATCTGCCTATCTGATTACATAGGGAAGACTGGGAATCTGCTGCTGGTGGCGGCCCACTCTCACAGG  
GAGCAGATCAGCAGAGGTGCTGGAGTTGGAGATACAGCTGGGCCAACATCAGTCCAGGCCACAGACAGCGGCGCGAC  
GAGGAGAATGCTTACACAAGATGAGCACTTCCGAGCTCTGAGCCTCTGGCCGCTCTCATGATGACTGGCTTGTAGTCT  
CTGCTTCTTCTGCTGCTACCTTAGGTTGAGTAGTCTGAGCTCTGAGCTGTGGTGTTGATGGATGGATTTTGTTCAG  
CAGGTTGCAAGCTCATCAACCGCACAGGACCAAGCATCTGGAACAATTACTGATCTGGAACCTGTGTGGCAAGAG  
ACAACTCAGAGCTGGACCGACCTTTGAGTCTGACACAGAGAAGCTCTGGAGAGCTCTATGGCACAAGAAAG  
TCTGTTGTGCGCAGGCTGGACAGCTGCATCTCAACACGGAATGACGCCCTTGGCTTGTCTTTGGGGTCACTCTTC  
TGAGAGCGCTCGTTTGAACCGGCAAGAAAGAATTGACAGAGGGATGATCAGCGAATCCCGACCGCATTTGAG  
GAGGCTCGTGGGACAGCTGTTTGGATGGATGAGAAGACCGCCGACGACGACGAGCAAGGAGAAGACGATGGCACTTAT  
GATATGATTGGTTTCCCAAGATCTCTCGAGCGCAAGAAGACTGATATGATTTATGACGGGTACAGAAATTTCT  
GAAGATCTCTTCTTCCAAAGATGTTGAAATTTGTACAACCTTCTGGCAAGTATAGGCTGACCACTCTCGGACAG  
CTCTCCGACGGAGACAGCTGAGACATGACCCCGACAGCAGTGAATGCGTACTACCTTCAACAATAAGAAATGAGATC  
GTCTCTCCCGCTGGCATCTGCTCAGGCGCCCTCTCTTCTCGGCAACACCCCAAGGGCCGAACTTCTGGTGAT  
GTTGTGTCTATGGCGCATAGTTTATGCATGATCTTATGATACAAGGCGCGAGATGACAAAGAAGAAACCTG  
CGCCGCTGGTGAGAGATGAGTCTCGGACGCTTCCGGAAACACACGGCCTGATAGGAGAACAGTACAATCACT  
TACAGGCTCAATGGGAGAGGCTCAACGGCGGACAGAGCTGGGGGAGAAATTACTTGGACGACCGGGGCTGAA  
GCTGCCCTACAATGCTTACAAGAGCTGCTGAGAAGAGCATGGGAGAGGAGCAGCACTCAGCGCGTGGGCTCACC  
AACCCACAGCTCTTCTTCTGTGGGATTTGCCAGCTGTGGTGCTCTCGTGGCGACACAGAGAGCTCTACAGAGGG  
CTGTGTGACCGAACCCAGACAGGCTGCGCGCTCTCGCGTGTGGGCATCTCTCAACTCCCGGTGACTCTCTCGG  
CACTTCTCGGCTGCGCTGTGCGCTTCCCATTGAACCCAGGCGACTGTGTGAGTGTGGTAGACCTGATCAGGGGA  
GAAATGSCCAGCTGTGACAGCACTGGGCGACTCTCTCTACAAGGCTTTTGTGCTCTTGGGTTGGGAGGAAGCA  
ATTGACGCTGGGCTGGGCTGAGTCTGCTCCCCCAAGCTGATGATGACAGCCCTCTCAATACCAACTAT  
TGCTCTGCTTTGGGGGTGCCCTGCTCCAGCAGAGGCCCAACTCACTGTGACATCTTTCGTTGTCACCT  
CGCTGGAAGAGGTCTGGGTGGGAGGCCGATTCCATAGGAAGGAGTCTGCG

## **FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVL TAY  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSFLVKATFDRQSKEIAEGMI  
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISED SF  
FQNMLNLYNPSAKVMADQLRKPPSRDQWSMTPTQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNPGGIGVVMGHELTAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHF GCPVGS PMNPGQLCEVW

### **Type II Transmembrane domain:**

amino acids 32-57

## FIGURE 226

GCCGCCCCCTCCGCCCTCCGCACTCCGCCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCCTCCCTCCCTCC  
 CAGCTGTCCCGTTCGCGCTCATGCCAGAGCCTCCGCCGCCCGCGGCCCCCGCTGCTCTCCCTGGGCTGCTGCTGCT  
 CGGCTCCGCCGCCCGGCCGCCGCCGCCAGAGCCCCCGGTGTGCTGCCATCCGTTCTTAGAAGAGAGCGCTGCC  
 CGTTCCGGGAGCGGCGAGTAGGTGGGGGCCCGGGGGAGGCGCGGGCGGGAGTCCGGCTCCGGGCGAGTCAAGCGC  
 CAGCCCCGAGGGGGCGCGGGCGCAGGTGGCTCGCGCGCGCGCGCGCGCGCGAGAGGTGGCGCGGGCGCAGAAGGCG  
 CGGGTCTGGGACCCGGGAGCCCGCGGCGAGCCCCCGGGCGCGCACAACCGCGCAGCTGGGCGAGCGGCTCCAGC  
 CAAAGCGCTCCCCGAGAGCTCACTTCGGCGGGAAGTCTATGCTTGGACAGAGCTGGCACCCCGAGCTTAGG  
 GGAGCCATTCCGGGGTGAATGCGCTGCTGCTGTGCGCTCGAGGCGCAGTCAGTGGGGTCCGGTACCAAGGGCGTGG  
 CAGGCTCAGCTCAAGAACTCAAAACAGAGTGCCCAACCCCGGCTGTGGGCGAGCGCGCAGCTCCGGGACCA  
 CTGCTGCGCAGAGCTCCGCCAGCACTTCGTGGCGCTGTGACAGGCGCGAGTGGCTCGCAGGCGGTGCGCAGAGCCCG  
 AGTCTGCTGCTGCGCTCTAGCTCTCGCTTCTATCTCTACAGGCGGCTGGACCGCCCTACACAGGATCCGCTT  
 CTCAGAGCTCCAATGGCAGTGTCTGTTTGGACACCCCTGCAGCCCCCAACCAAGATGGCTGGTCTGTGGGGTGTG  
 GCGGGCAGTGCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA  
 CCTTCCAGGGGAGGTCTGGGGGCTCATCCGCGACCGGGCCCTGTCCCAAGAGACTTCAGTGCCATCTGAC  
 TCTAGAAGGCCCCCAACGAGGGGCTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA  
 TTTTGTGCTCTCTCCGAGGCTTGCAGGACTAACCCAGGTTCCTTGAGGCTCCAGATTCTACACCGAGGCA  
 GCTACTCGAGAACTTCAGGCCAATGTCTCAGGCCAGGAACAGGCTTGTGAGGTTGCTGCCAACCTGACAT  
 CCAGGAGATGGACTGGCTGTGCTGGGGAGCTGCAGATGGCTGGAGTGGGCGAGCGAGGCGTGGCGAT  
 CAGTGGAACACATTGCTGCGAGGAAGAGTGCAGCGTCTCGCAAAGTGTCTTGTGGGGCTAATGCCCTGATCCC  
 AGTCCAAACGGGTGCTGCGGCTCAGCCAGCCTCACTCTGCTAGGAATGGGCCCTGATCTCCAGGTGCAATT  
 GTTAGGGAACAACAGTGAAGTGGTGCCATGACACTGGAAACCAAGCCTCAGCGAGGAGTACAGCCACTGTCTCT  
 GTGCCACATGGCTGGCCCTATCTCCCTGCCCGCCAGCGCGTGGGTATCTGCGCTGGGCTGGGGTCCCGAGGGC  
 TCATATGCTGCTGCGAATAGCTCTCTCTGAACGTGGGCAACAGGACTCCCAAGCGGAGAGCTTCCGGGGCA  
 ACGTGCGTCCCTGCGCTCTGTGGGGCATAGCGCCGCTGCCCGTCCCTAGCAGAGAGCCTGTGGTGCTAC  
 CCGTGTGAAGAGCCAAAGCAGCAGGGCAGCCTGGCTTCTTGGATACCACTGTCACTGCACTATGAAGTGTCT  
 GCTGGCTGGGCTTGGTGTGCTCAGAACAGGCAGTGTCACTGCCACCTCTCTGGGCGTGGGAGCGGAACTGCTGCG  
 TCGCGGCTGTGAAGGGATTCTATGGCTCAGAGGCCAGGGTGTGGTGAAGGCTGGAGGCGGAATGCTGCG  
 GCACCTGCAAGAGCTATGGCTGATGATCAACCAAGTACCCACAGAGGGAGCTCCGAGGCGAGCTCT  
 CTCCTCCAGGTGACATAGCACAACCAATGTGAGGTGGCGGACTGCGCTGGAGGCGCGCGGGCGAGGGGGT  
 GCGGGCGCTGGGGCTCCGATACAGCCTCTGCTGCGCGGCTGTGGTGCCTGTGCTCCCGGCTAGCGGCCGCG  
 CAAAGTGTGGTGTCTGGGGCGCCCGAGAGCCCAACACATGCTTCTTCGAGGGGACAGCGCCGCCACCGGGG  
 TCGTGGGGCGCCAACTACACCCGCTCTGCTCACTTGCACCTGCCACAGAGCAAGCGTGATCTGTACCCGCT  
 GGTGTGCCACCGGCCAGCTGGCCCAACCCGGTGAAGGCTCCGACAGTGTCTGCTCTTGTGGCCCTGGCTGTCTA  
 TTTTGTGTTGTTGACCGAGGCTGGCGGGCAGGGGTACGCGGTGGCACCCCTTGTGGCCCCCTTGGCTTAATTA  
 GTTGTGCTGTCTGCACCTGCAGCAGGGGGGCACTGGAGAGGTGCACTGTGAAGAGGTGAGCTGTCCCGGCTGGC  
 CTGTGCCAGCCTGTGGCTGTCAACCCACGACTGCTGCAACAGTGTCAAGTGAAGCCCAACCCAGCTGGG  
 GGACCCCATCGAGCTGATGGCGCCCGGGCTGCCCTTGTGCTGGCAGTGTTTCCAGAGGCTCAGAGCTGGCA  
 CCCCTCAGTCCGCCCTTGGAGATGAGCTGTATCACTTCGAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT  
 GTGAGGTGGGTACTGGGAGCTCTGAGATAGGAGACTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA  
 CTGTCTCCCACTGCTCTCTGGGGGCACTCAGTGTCTGTCTGTGATCAGGCGAGGGTGTGCTCACTGTGAGC  
 GGGATGACTGTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGTGTTCCGCTGTCAGCGGCCACC  
 GCGCGGCTAAGTGAAGGAGTGCAGAGTGCAGCTGTGAGTGAAGGGCTCACTGCTGTGGAGCTCCGTATGAC  
 GGAAGGAGGCACTCACTGTGTGCGGGAACAGTGCAGCGTCCCTCAACAAGTGCATTCACCTCAGACGAC  
 ACCTGTGGAAATTTATTTATGACCTTTTCTTCAAAATGAGATTTCGAAGCTCAGAGAATTAAGACAAGAG  
 ATGAAGATCCAGAGCTGTGTGCACCTGACCTGTTTAGAAAATATGGCTTTCTGGGACCAAGCGAGGATGCTT  
 TGCCCTGCCCTCTATGCGCTCTGTGGCTCTCCACTCCCTCTCCCTCTCCCAATTCCTCCCTCTGTGCTCC  
 AGCAGCCCGAGAGCCAGAACTGTCCAGAGCTGGAGAAAGAAAGCGAAGGCTTAGGGGAGCTCCAGCGAGGCC  
 AAGTGAACAGAGAGGATGGGGCTGAGCTGGGGAAAGGGTGGCATCGAGGACCTTTCGATCTTCCTGTGGGAAG  
 CCGAGTGCCCTTGTCTCTGTCTGCTCTACTCCCAACCCCACTCACTCTGGGAACCAAGCTCACAAGAGGG  
 GAGAGGCACTGGGCGCAACCGAGGTCAAGCCACTCCAAGTCTGCTGCCACCTCGGCTCTGTCTCGGAA  
 GCGCCACCCCTTCTTCTGATACAAATGTCACTGGCTTGTGGGATTTTAAATTTATCTCACTCAGCAACGA  
 GGCCCGGCACTCACTCTGCTGCCCTGAGCTGAGCAGAGTCATTATTTGGAAGTGTGATATTTATTAATAAAC  
 ATTTCTTTTTCAGTCTTTGGGACAGTGGTGGCTCTTTGTGGCCAGGAACCTGAGTGGGCGCTGGTGGAGAGG  
 CGNGAGAGTAGGAGGTGAGAGAGGAGGAGCTGTGACACTTGGGAGCTGAAAGAGACCTGGAGAGGCGAGAGGAT  
 GCGGCGNNTTGGCTGAGCANCTTGGGTTCCGACAGGGGCTGGGGATGGTTCTTGAGATGGTGTAGAGACTCAAG  
 AATTTAGGGAAGTAGAAGCAGGATTTGACTCAAGTTAGTTTCCACATCGCTGGCCTGTTTGTGACTTCATG  
 TTTGAAGTTGTCTCCAGAGAGGAATCAAAGGTGTCAACAGCCCTCTCCCTCCCTCCCTCCCTTCCCTTCTC  
 TTCCTCCCTCCCTCCCTCCCTCCCTCCCTCC

0078101.101501

## **FIGURE 227**

GGCCGAGCGGGGTGCTGCGCGCGGCCGTGATGGCTGGTGACGCGGGGCGGGGAGGGGA  
CGGGGGCCGCGGCCCGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC  
TCCACCATGAACGTTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAATAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGTGGATTGCGA  
GGAACCCCTGCCCAGTGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAATAACACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGTTCTACCTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACCTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCCTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCATCCCTACCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTCTTCTCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTTCTTCT  
TCTTATTCTTCTAGTAGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTGCG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAAGGGTCTGAGGATTGAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAAGAGATTGCATTGAGCCAGGTCTGTAG

## FIGURE 228

ATGCCTACTACCTTCCAACATAAGAAATGAGATCGTCTTCCCCGCTGGCATCTGCAGGCCCCC  
TTCTATGCCCGCAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGC GGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTGGTCCGCACACCAGAGAGCTCTCACAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAATCCCGTGACTTCCTGCGGC  
ACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGATCAGGGGAGAAATGGCCAGCTGTACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTGGGAGGAAGCAAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCTCTCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCTT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGGCTCACT  
CAGCCTGGCGCCCATGGGGCCTGCCGTGCCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCAGGCTCACTCAGTGCCTACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTACCCCTCACGGGCTACCCCCACCTCACCCCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAAATGATTGATTCTCCTTGGACAAAGCAGGAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

## FIGURE 229

CCCCGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAAGCAACCGAGA  
GGAGGGGAGGCCAAAAACCCGAAAAACAAAAAGAGAGAAACACCCCAACCACTGGGGTGG  
GGGGAGAGAAAGAAAGAAAGAAACCCACCCACCCAAAAAAGAAAAAAGAAAAA  
AAAAAAGAAAAATCCTGTGGCGCGCGCCTGGTTCCCGGGAAGACTCGCCAGCACCGGGGG  
TGGGGAGAGTGCAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
CTGTTGGTGCAGGGTGTCTGTTGCTCGAACCACTGGCTGGCGCGGTGCTCCTCAGCCTGTG  
CTGCCTGCTACCCCTCTGCTCCCGGCTGGACAGAGTGTGGAATCCCTGGCGGCGGTGG  
ACAAATGATGGTGCAGAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTGGCGGGAGGTGATAAGTGGTCAGT  
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTGAGTCAACATACACCCAGAACA  
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACAGAGCCTTCCA  
TTTCTTGGCGACACATCTCCCATCAGCAAAACCAATTGAAATGGACAATATTTGGACATT  
TATGGAATTAACAGGACACAGGTGCGGCTGGAATGCAATGCAGCGGAAATGCTGTGTCAAT  
CCCAGATGTGAGGAAAGTAAAGTGTGTGCAACTTTGCTCCTACTATTACAGGAAATTAAT  
CTGGCACCGTGCACCCCGACGCGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
CCAGCCTTTGAATGGTGACAAAGGAGAGAGAAGAAGCTCTTCAATGGCCAAAGGAATTTAT  
TCAAAATTTTAGCAACAAGATCCATTCTACTGTTACCAACGTGACACAGGAGCACTCTGGCA  
ATTATACCTGTGTGGCTGCCAACAGCTAGGCAACAACCAATGCGAGCTGCTCTTAAACCT  
CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT  
TGTGTTGACACTGTCCTCTTCCAGCATATTCTACTGAAGAATGCCATTCTACAATAAA  
TTCAAAGACCCATAAAAGGCTTTAAGGATTCTCTGAAAGTCTGATGGCTGGATCCAATCT  
GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGATGATCGCC  
TTCTGTAGAATTGCTCATTTAGTAAATACTTAATTCTACTCTTTTGTATTAGTACATTA  
CCTTGTGAAGCAGTACACATTGTCTTTTAAAGACGTGAAAGCTCTGAATACTTTTAG  
AGGATATTAATTGTGATTTCATGTTTGTAAATCTACAACCTTTTCAAAGCATTCAGTCATGTT  
CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAAGTGAATGTGATTCTTTAA  
GGCTGCAATACAAGCATTGAGTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAGATG  
CATTTTTTTCTTTTGTAAAAAAGCAAATAATATTGCCCTTCAGATTATTTCTTCAAATA  
TAACACATATCTAGATTCTTCTGCTTGCATGATATTCAAGTTTCAGGAATGAGCCTTGTAA  
ATAACTGGCTGTGACGCTCTGCTCTCTTCTGTAAGTTTCAGCATGGGTTGCTCTCATAC  
AATAATATTTTCTCTTTGTCCTCCAACATAATAAAATGTTTGTCTAAATCTTCAATTTGA  
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACATCTCTAAAGTAACGAAGGAGC  
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAAGATTTTGGCCACACT  
AACTCAGTTCTGTGATGAGAGACAATTTAATAACAGTATAGTAATATCCATATGATTTT  
TTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA  
GTCCACTCAAAGGATTGCCTAGCAATACAGATCTTTTCTTTTCACTAGTCCAAGCCAAAA  
TTTTAAGATGATTTGTGAGAAAGGGCAAAAGTCTATCACCTAATATTACAAGATTGGTA  
AGCGCTCATCATTAATTTATTTTGTGGCAGGTATTATGACAGCTGCACCTGGAGGGTATGGA  
TATGATATTGAGAGCTTCCAGGACTATAATGGCAGAAAACGAGGTGTTATGAGCCTATC  
AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA  
CAAGGAATAATTTCTGATCCAGGATCGTCTTCAAATGGCTGTATTTATAAAGGTTTGTG  
AGCTGCACTGAAGACTCTTATTTTATAGTATCAACCTTTTGTATTTTAAATTTGACCTGCCA  
AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
AGACAATTTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLN RSSIIFAGGDKWSVDPRVSI STL NKR DYS LQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYEC SAENAVSFDPVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLSSTSI FYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

## FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCAACAAGCTGCTTTTACCAGAAATGCAATGGAGCCTTTTCGAAA  
TCAATGTTCCAAAGCCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCTGGAGATGTATTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCTGGAGAACCTGGCTCAGGGTGATCGAGGCTG  
CAAGTCTGCAGGCCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGTCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTACAAGGGGCCATGGGCATGCCTGGTGCCTTGGCCCGCCGGGACCACTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAGGACCCCAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCAAAAGGGGAACTTGAAGTAAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGTTCATGGGGCTCTCGGAGCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTCCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCGGGCCCTCTGGTGCAGTGGGACACCAGGTGC  
CAAGGTGTAGCCTGGCAGTGTCTGGCTCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAGAGGTGAAAACCTCAGTGTCC  
GTCAGGATTGTGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAGTGTCTGGGGCAGCGAGAGTACCCTGTGGAGCTGCACCAAGAAATAGCTGGGGCCATCA  
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGCTTGAAGCCCGAAACCCCTTCA  
CTTCTCTGCTCCCGAGGTGTCTCTGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

## **FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGA MGMPGAPPPGPPAEKGAKGAMGRD  
GATGPPSGPQGPVGKGEAGLQGPQGAPGKQATGTTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGD LGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGA KGDQGGPGLQGVPG  
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGD TGLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWL DNVQCRGTESTLR  
SCTKNSWGHHDSCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

## **FIGURE 233**

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAGGAAAGAAGAAAAAGGCCAAAGCCAAAATGAAACTGATGGTACTTGTTTTCAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG  
TGATTCCTTGCAACAATCAATGAAGAATCTTCATGTATTCTGGAGAACACCATTTCCTGATTTT  
CCACAAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA



## **FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

# FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCAGCCTCGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTGGAGGGC  
 CGCAGTAGACGACGACGACGCGCGGGTCCCGGGAGGCCGCTCTGCTCGCGCCGAGATG  
 TGGAACTCTCCTTACGAAACCGACTCGGCTGTGGCCACCGCGCCGCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTA  
 TAAAATCCTCCAATGAAGCTACTAACATTACTCTCAAAGCATAATGAAAGCATTTTTGGAT  
 GAATTTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATTACCACATTTAGC  
 AGGAACAGAACAACACTTTCAGCTTGCAAAGCAAATTCATCCAGTGGAAGAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTTACCACAAATAGACTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC  
 AAGGAATGCCAGAGGCGGATCTAGTGTATGTTAACTATGCAACGAACTGAAGACTTCTTTAA  
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGT  
 TTTTCAGAGGAAATGAAGTTTAAAATGCCAGCTGGCAGGGGGCAAAGGAGTCATTCTCTACT  
 CCGACCTCGCTGACTACTTGTCTCTGGGGTGAAGTCTTATCCAGACGGTTGGAATCTTCTCT  
 GGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC  
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGAATTCAGAGGCTGTTGGTCTTCCAA  
 GTATTCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC  
 TCAGCACCACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGG  
 CTTTACTGGAACCTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA  
 CGAGAATTTACAATGTGATAGGTAATCTCAGAGGAGCAGTGAACACAGACAGATATGTCATT  
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATTTGTAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
 CAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTTATGAAAGTTGG  
 ACTAAAAAAGTCTCTCCACAGAGTTTCAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG  
 AAATGATTTTGAGGTGTTCTTCCAACGACTTGAATTTGCTTCAGGCAGAGCACGGTATACTA  
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACTCTACTGTGGCCACAGGTTCG  
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGTCTCCCTTTTGATTGTGCGAGATTATG  
 CTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCATAGTATTAAAGAA  
 TGATGAATCATCACTCATGTTTCTGGAAGAGCAATTTATTGATCCATTAGGGTTACAGCA  
 AGGCCTTTTATAGGCATGTATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC  
 ATTCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCCTTCCAAGGCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAAGTGCAGGCGCTGCAGAGACT  
 TTGAGTGAAGTAGCCTAAGAGGATTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA  
 CTCAGAAAGATCGTAATGGTATATTGATAAATTTTAAAATTTGGTATATTGAAATAAAGT  
 TGAATATTATATATAA

10073101.101501

## **FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL  
DELKAENIKKFLHNFTQIPHLAGTEQNQFLAKQIQSQWKEFGLDSELAHYDVLLSYPNKTH  
PNYISIIINEDGNEIFNTSLFEPPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVIARYGKVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV  
ILGGRHRSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAAEEFGLLGSTEW  
AEENSRLQLQERGVAIYNADSSIENYTLRVDCTPLMYSLVHNLTKEKLSPEDEGFEKGLYES  
WTKKSPSPEFSGMPRISKLGSNDFEVFFQRLGIASGRARYTKNWEKNKFSGYPLYHSVYET  
YELVEKIFYDPMFYKHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTVSVSFDLSLFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHVIYAPSSHNYAGESFPPIGYDALFDIESKVDPSKAWGEVKRQIYVAFTVQAAAE  
TLSEVA

### **Signal sequence:**

amino acids 1-40

### **N-glycosylation sites.**

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### **Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

### **N-myristoylation sites.**

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713